

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 14:51:15 ; Search time 1426 Seconds
(without alignments)
1550.137 Million cell updates/sec

Title: US-10-068-067-16
Perfect score: 51
Sequence: 1 ggtaccactggtctcttctgt.....caagaacttatcgaaataca 51

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_hg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sv.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_on.*
- 21: em_ov.*
- 22: em_pat.*
- 23: em_ph.*
- 24: em_pl.*
- 25: em_ro.*
- 26: em_sts.*
- 27: em_un.*
- 28: em_vi.*
- 29: em_hg_hum.*
- 30: em_hg_inv.*
- 31: em_hg_inv.*
- 32: em_hg_inv.*
- 33: em_hg_mus.*
- 34: em_hg_pln.*
- 35: em_hg_rod.*
- 36: em_hg_mam.*
- 37: em_hg_vrt.*
- 38: em_sy.*
- 39: em_hgo_hum.*
- 40: em_hgo_mus.*
- 41: em_hgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	51	100.0	51	6	AX513217	Sequence
2	51	100.0	51	6	AX513222	Sequence
3	51	100.0	348	9	AF262299	Homo sapi
4	51	100.0	957	9	AF224496S1	Homo sapi
5	51	100.0	1453	9	AF247360	Homo sapi
6	51	100.0	2895	6	AX513212	Sequence
7	51	100.0	2895	9	AF237380S1	Homo sapi
8	51	100.0	177334	9	AC138069	Homo sapi
9	51	100.0	197279	9	AC104439	Homo sapi
10	51	100.0	220965	2	HSJ12688	Homo sapi
11	49.4	96.9	1454	9	AF247359	Homo sapi
12	48	94.1	260	9	AF224495	Homo sapi
13	48	94.1	406	9	AF262301	Homo sapi
14	48	94.1	410	9	AF262302	Homo sapi
15	47	92.2	212	9	AF262303	Homo sapi
16	47	92.2	436	9	AF262304	Homo sapi
17	35	68.6	1193	6	AR300122	Sequence
18	35	68.6	1193	6	BD082061	G-protein
19	26.4	51.8	41270	3	CEI1086	Z21491 Caenorhabdi
20	25.8	50.6	3892	12	ECCFVIAH	Z21706 E.coli/C.fr
21	25.8	50.6	7907	1	AY282413	Citrobact
22	25.8	50.6	17007	1	AF316551	Citrobact
23	25.6	50.2	21362	2	AC130869	Rattus no
24	25.6	50.2	276975	2	AC106673	Rattus no
25	25.4	49.8	31059	9	AC009005	Homo sapi
26	25.4	49.8	32074	9	AC011556	Homo sapi
27	25.4	49.8	292420	2	AC020873	Mus muscu
28	25	49.0	174069	2	AC026852	Homo sapi
29	25	49.0	177929	9	AC125624	Homo sapi
30	24.6	48.2	1533	3	AK116158	Ciona int
31	24.6	48.2	69334	2	AC007778	Homo sapi
32	24.6	48.2	181250	9	AC090403	Homo sapi
33	24.6	48.2	181712	2	AF001103	Homo sapi
34	24.6	48.2	184026	9	AC022176	Homo sapi
35	24.6	48.2	186458	5	AL929391	Zebrafish
36	24.6	48.2	191312	2	AF001030	Homo sapi
37	24.6	48.2	194633	2	AC090362	Homo sapi
38	24.4	47.8	323	11	KLJ9884	Kluyverom
39	24.4	47.8	157325	9	AC027189	Homo sapi
40	24.4	47.8	163157	9	AC099784	Homo sapi
41	24.4	47.8	231772	2	AC117860	Rattus no
42	24.4	47.8	259236	2	AC123741	Mus muscu
43	24.2	47.5	157190	8	NCB18D24	Neurospor
44	24	47.1	218710	2	AC147438	Gallus ga
45	24	47.1	233527	10	AC124576	Mus muscu

ALIGNMENTS

RESULT 1	AX513217	51 bp	DNA	linear	PAT 03-OCT-2002
AX513217	Sequence 16 from Patent WO02062848.				
LOCUS	AX513217				
DEFINITION	Sequence 16 from Patent WO02062848.				
ACCESSION	AX513217				
VERSION	AX513217.1	GI:23504280			
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens				
REFERENCE	1				
AUTHORS	Rotherberg, M.E. and Zimmerman, N.				
TITLE	Regulation of cc chemokine receptor 3 (ccr3) expression				
JOURNAL	Patent: WO 02062848-A 16 15-AUG-2002;				

CHILDREN'S HOSPITAL MEDICAL CENTER (US)

FEATURES
source

Location/Qualifiers
1. .51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 51; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 4.9e-09;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTACCACTGGTCTTCTGTGCTTATCCGGCGCAAGAACTTATCGAAATACA 51
|||||
Db 1 GGTACCACTGGTCTTCTGTGCTTATCCGGCGCAAGAACTTATCGAAATACA 51

RESULT 2
AX513222 100.0%; Score 51; DB 6; Length 51; PAT 03-OCT-2002
LOCUS AX513222 51 bp RNA linear
DEFINITION Sequence 21 from Patent WO02062848.
ACCESSION AX513222
VERSION AX513222.1 GI:233504285

KEYWORDS
SOURCE

Homo sapiens (human)
Homo sapiens

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 Rothenberg, M.E. and Zimmerman, N.
Regulation of cc chemokine receptor 3 (ccr3) expression
Patent: WO 02062848-A 21 15-AUG-2002;
CHILDREN'S HOSPITAL MEDICAL CENTER (US)

FEATURES
source

Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

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Best Local Similarity 100.0%; Pred. No. 4.9e-09;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTACCACTGGTCTTCTGTGCTTATCCGGCGCAAGAACTTATCGAAATACA 51
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Db 1 GGTACCACTGGTCTTCTGTGCTTATCCGGCGCAAGAACTTATCGAAATACA 51

RESULT 3
AF262299 100.0%; Score 51; DB 6; Length 51; PRI 26-JUN-2002
LOCUS AF262299 348 bp mRNA linear
DEFINITION Homo sapiens clone 1 CC chemokine receptor 3 (CCR3) mRNA, partial cds.

ACCESSION
VERSION

AF262299
AF262299.1 GI:19171640

KEYWORDS
SOURCE

Homo sapiens (human)
Homo sapiens

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 348)
Vijh, S., Dayhoff, D.E., Wang, C.E., Iman, Z., Ehrenberg, P.K. and Michael, N.L.
Transcription Regulation of Human Chemokine Receptor CCR3: Evidence for a Rare TATA-less Promoter Structure Conserved between Drosophila and Humans

JOURNAL

Genomics 80 (1), 86-95 (2002)

MEDLINE

22074933

PUBMED

12079287

REFERENCE

2 (bases 1 to 348)
Vijh, S., Dayhoff, D.E., Wang, C.E., Ehrenberg, P.K. and Michael, N.L.
Direct Submission

JOURNAL

FEATURES
source

Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis,
Walter Reed Army Institute of Research, 1600 E. Gude Drive,
Rockville, MD 20850, USA.

Location/Qualifiers

1. .348
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="3"
/map="3p21"
/clone="1"
/cell_type="eosinophil"

gene

1. .>348
/gene="CCR3"

CDS

120. .>348
/gene="CCR3"

/note="G-protein coupled receptor; principal eosinophil receptor expressed on eosinophils, CD4 Th2 lymphocytes, CD8 lymphocytes, microglia, dendritic cells, and monocytes"

/codon_start=1
/product="CC chemokine receptor 3"

/protein_id="AAU85628.1"

/db_xref="GI:19171641"

/translation="MTISLTIVETFGTTSYDDVGLLCEKADTRALMAQFVPPYLSIV
FTVGLLGNVVVVMILIKIRLRIMTIYLLNL"

ORIGIN

Query Match 100.0%; Score 51; DB 9; Length 348;
Best Local Similarity 100.0%; Pred. No. 4.5e-09;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTACCACTGGTCTTCTGTGCTTATCCGGCGCAAGAACTTATCGAAATACA 51
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Db 27 GGTACCACTGGTCTTCTGTGCTTATCCGGCGCAAGAACTTATCGAAATACA 77

RESULT 4

AF224496S1

LOCUS

AF224496S1 957 bp DNA linear PRI 02-MAY-2001

DEFINITION

Homo sapiens CC chemokine receptor 3 (CCR3) gene, exon 1.

ACCESSION

AF224496
AF224496.1 GI:13924485

VERSION

AF224496.1 GI:13924485

KEYWORDS

1 of 2
Homo sapiens (human)

SEGMENT

Homo sapiens

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 957)
Scotet, E.J.

AUTHORS

CCR3 expression is associated with chromatin remodeling in Th2 cells

TITLE

Unpublished

JOURNAL

2 (bases 1 to 957)
Scotet, E.J.

AUTHORS

Direct Submission

TITLE

Submitted (13-JAN-2000) Basel Institute for Immunology, 487
Grenzacherstrasse, Basel CH-4005, Switzerland

JOURNAL

Location/Qualifiers

1. .957
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

FEATURES
source

298. .376
/gene="CCR3"
/note="exon 1"

exon

100.0%; Score 51; DB 9; Length 957;
Best Local Similarity 100.0%; Pred. No. 4.4e-09;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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Qy 1 GGTACCACTGGTCTCTTGTGCTTATCCGGGCAAGAACTTATCGAATAACA 51
Db 295 GGTACCACTGGTCTCTTGTGCTTATCCGGGCAAGAACTTATCGAATAACA 345

RESULT 5
AF247360 1453 bp DNA linear PRI 26-JUN-2002
DEFINITION Homo sapiens CC chemokine receptor 3 (CCR3) gene, promoter region
and partial sequence.
ACCESSION AF247360
KEYWORDS AF247360.1 GI:19110541
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1453)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Inam,Z., Ehrenberg,P.K. and
Michael,N.L.
TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence
for a Rare TATA-less Promoter Structure Conserved between
Drosophila and Humans
JOURNAL Genomics 80 (1), 86-95 (2002)
MEDLINE 22074933
PubMed 12079287
REFERENCE 2 (bases 1 to 1453)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
TITLE Direct Submission
JOURNAL Submitted (21-MAR-2000) Dept. of Mol. Diag. and Pathogenesis, U.S.
Military HIV Research Program, 1600 E. Gude Drive, Rockville, MD
20850, USA
FEATURES
source
Location/Qualifiers
1..1453
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/map="3p21; between CCR1 and CCR5"
/clone="A8"
/cell_type="peripheral blood mononuclear cell"
1..>1453
/gene="CCR3"
755
variation
/gene="CCR3"
/mrna
/replacement="t"
822..>1453
/gene="CCR3"
/product="CC chemokine receptor 3"
exon
822..1163
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variation
1114
/gene="CCR3"
/replacement="g"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 4.3e-09;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTACCACTGGTCTCTTGTGCTTATCCGGGCAAGAACTTATCGAATAACA 51
Db 1082 GGTACCACTGGTCTCTTGTGCTTATCCGGGCAAGAACTTATCGAATAACA 1132

RESULT 6
AX513212 2895 bp DNA linear PAT 03-OCT-2002
LOCUS AX513212
DEFINITION Sequence 11 from Patent WO02062849.
ACCESSION AX513212
VERSION AX513212.1 GI:23504275
KEYWORDS
SOURCE Homo sapiens (human)

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Rothenberg,M.E. and Zimmerman,N.
TITLE Regulation of cc chemokine receptor 3 (ccr3) expression
JOURNAL Patent: WO 02062848-A 11 15-AUG-2002;
CHILDREN'S HOSPITAL MEDICAL CENTER (US)
FEATURES
source
Location/Qualifiers
1..2895
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Query Match 100.0%; Score 51; DB 6; Length 2895;
Best Local Similarity 100.0%; Pred. No. 4.2e-09;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTACCACTGGTCTCTTGTGCTTATCCGGGCAAGAACTTATCGAATAACA 51
Db 1561 GGTACCACTGGTCTCTTGTGCTTATCCGGGCAAGAACTTATCGAATAACA 1611

RESULT 7
AF237380S1 2895 bp DNA linear PRI 05-OCT-2000
LOCUS AF237380S1
DEFINITION Homo sapiens CCR3 gene, promoter and exon 1.
ACCESSION AF237380
VERSION AF237380.1 GI:10643652
KEYWORDS
SEGMENT 1 of 2
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2895)
AUTHORS Zimmermann,N., Daugherty,B.L., Kavanaugh,J.L., El-Awar,F.Y.,
Moulton,E.A. and Rothenberg,M.E.
TITLE Analysis of the CC chemokine receptor 3 gene reveals a complex 5'
exon organization, a functional role for untranslated exon 1, and a
broadly active promoter with eosinophil-selective elements
JOURNAL Blood 96 (7), 2346-2354 (2000)
MEDLINE 20458773
PubMed 11001881
REFERENCE 2 (bases 1 to 2895)
AUTHORS Daugherty,B.L.
TITLE Direct Submission
JOURNAL Submitted (22-FEB-2000) Immunology & Rheumatology, Merck Research
Laboratories, 126 East Lincoln Avenue, Rahway, NJ 07065, USA
FEATURES
source
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/map="3p21"
/clone="350-3B"
/clone_lib="BglII fragment from phage P1 human genomic
library (DMPC-HFF No. 1; Genome Systems, Inc., St. Louis,
MO)"
1..1551
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33..38
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1287..1292
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/gene="CCR3"
1552..1642
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/notes="untranslated"
/number=1

ORIGIN

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Query Match 100.0%; Score 51; DB 9; Length 2895;
 Best Local Similarity 100.0%; Pred. No. 4.2e-09;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTACCACTGGTCTTCTGTGCTTATCCGGCGAAGAACTATCGAATAACA 51
 Db 1561 GGTACCACTGGTCTTCTGTGCTTATCCGGCGAAGAACTATCGAATAACA 1611

RESULT 8
 AC138069 177334 bp DNA linear PRI 19-FEB-2003
 LOCUS Homo sapiens chromosome 3 clone RP13-54612, complete sequence.
 DEFINITION
 AC138069
 ACCESSION
 VERSION
 AC138069.3 GI:28416170
 KEYWORDS
 HTG.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 177334)
 Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
 Saenphimmachak,C., Buckley,D., Kibukawa,M., Raymond,C. and
 Haugen,E.D.
 Direct Submission
 Unpublished
 2 (bases 1 to 177334)
 Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.
 Direct Submission
 Submitted (12-DEC-2002) Genome Center, University of Washington,
 Box 352145, Seattle, WA 98195, USA
 REFERENCE
 3 (bases 1 to 177334)
 Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.
 Direct Submission
 Submitted (10-JAN-2003) Genome Center, University of Washington,
 Box 352145, Seattle, WA 98195, USA
 REFERENCE
 4 (bases 1 to 177334)
 Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
 Saenphimmachak,C., Buckley,D., Kibukawa,M., Raymond,C. and
 Haugen,E.D.
 Direct Submission
 Submitted (19-FEB-2003) Genome Center, University of Washington,
 Box 352145, Seattle, WA 98195, USA
 JOURNAL
 TITLE
 On Feb 19, 2003 this sequence version replaced gi:27573398.
 COMMENT
 ----- Genome Center
 Center: University of Washington Genome Center
 Center Code: UWGC
 Web site: <http://www.genome.washington.edu>
 Contact: wgchtgs@u.washington.edu
 ----- Project Information
 Center project name: Chr-3
 Center clone name: RP13-54612 (bc0820)
 ----- Summary Statistics
 Sequencing vector: plasmid; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 177210 bases at least Q40
 Consensus quality: 177313 bases at least Q30
 Consensus quality: 177334 bases at least Q20
 Insert size: 177334; sum-of-contigs
 Quality coverage: 9.3x in Q20 bases; sum-of-contigs

 Overlapping Sequences:
 5': RP11-793E15 (UWGC:bc0564) AC104439, 95469-bp overlap
 3': U95626, 42710-bp overlap

 Sequence Quality Assessment:
 This entry has been annotated with sequence quality
 estimates computed by the Phrap assembly program.
 All manually edited bases have been reduced to quality zero.
 Quality levels above 40 are expected to have less than
 1 error in 10,000 bp.
 Base-by-base quality values are not generally visible from the

GenBank flat file format but are available as part
 of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:
 all regions were either double-stranded or sequenced with an
 alternate chemistry or covered by high quality data (i.e., Phred
 quality >= 30); an attempt was made to resolve all sequencing
 problems, such as compressions and repeats; all regions were
 covered by at least one plasmid subclone or more than one M13
 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest
 fingerprinting. Comparison of the experimentally derived digest
 fragments with sequence-predicted fragments is given below.
 The electronically-digested sequence consists of both insert and
 vector, in order to accurately represent the entire circular BAC.
 Small fragments below a variable cutoff (approximately 400-800 bp),
 are not resolved in the fingerprint and hence do not appear
 in the table. There are no significant remaining discrepancies
 between the experimental and predicted values. Uniquely ordered
 fragments are separated by dashed lines.

EcoRI

HindIII

BglII

SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt
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1239	1199	11125	10952	6306	6319
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449	<800	2290	2310	2067	2071
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510	<800	560	<800	3913	3756
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6511	6363	54	<800	2169	2210
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5296	5509	1159	1158	910	910
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10424	10027	4052	4034	875	893
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5046	5119	1846	1829	3716	3756
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1196	1199	8334	8273	4502	4523
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1397	1392	12882	12573	1967	1945
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2597	2624	448	<800	2864	2871
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3800	3818	10300	10103	4773	4738
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2248	2269	6671	6656	3707	3756
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1074	1055	4052	4034	336	<800
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7303	7718	1392	1386	79	<800
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959	959	4253	4286	4736	4738
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551	<800	2791	2834	1889	1945
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1074	1055	2647	2682	3696	3756
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5688	5759	3423	3409	1569	1539
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5183	5363	73	<800	8078	8038
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3100	3093	499	<800	1365	1325
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921	959	723	<800	289	<800
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4350	4244	2763	2834	11047	10790

4931	4857	6594	6556	8848	8963
3907	3818	4503	4468	1914	1945
8001	7718	5154	5136	1336	1325
3804	3818	4730	4713	11485	11341
2355	2376	13628	13324	974	975
862	868	166	<800	2448	2501
1711	1674	9554	9494	373	<800
5672	5759	1398	1386	1003	975
3900	3818	1613	1641	1787	1756
1905	1854	1479	1503	857	883
7872	7718	1540	1503	1974	1945
1174	1155	520	<800	1707	1631
7015	7139	219	<800	3835	3756
2852	2868	1571	1503	6586	6551
221	<800	154	<800	178	<800
1002	1055	5077	5136	2905	2871
201	<800	2156	2190	2500	2501
6717	6864	1075	1089	389	<800
237	<800	162	<800	41	<800
2737	2749	2752	2834	685	<800
3448	3416	1647	1641	2598	2662
3256	3238	7059	7056	248	<800
5801	5759	1547	1503	2152	2210
1512	1497	5163	5136	431	<800
1398	1392	8679	8719	237	<800
8413	8333	2033	2035	3380	3411
6621	6614	886	892	5694	5744
645	<800	---	---	3255	3265
1026	1055	---	---	183	<800
14333	14484	---	---	3128	3144
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Query Match 100.0%; Score 51; DB 9; Length 177334;
Best Local Similarity 100.0%; Pred. No. 3.6e-09;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACACTGGCTTCTTGTGCTTATCCGGGCAAGAACTATCGAATACA 51
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DB 65693 GGTACACTGGCTTCTTGTGCTTATCCGGGCAAGAACTATCGAATACA 65743
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RESULT 9
AC104439 197279 bp DNA linear PRI 20-JUN-2002
Homo sapiens chromosome 3 clone RP11-793E15, complete sequence.
AC104439 AC024739
AC104439.2 GI:21490240
HTG.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 197279)
Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
Saenphimmachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond,C.
and Haugen,E.D.
Direct Submission
Unpublished
2 (bases 1 to 197279)
Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.
Direct Submission
Submitted (11-DEC-2001) Genome Center, University of Washington,
Box 352145 Seattle, WA 98195, USA
3 (bases 1 to 197279)
Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
Saenphimmachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond,C.
and Haugen,E.D.
Direct Submission
Submitted (20-JUN-2002) Genome Center, University of Washington,
Box 352145 Seattle, WA 98195, USA
On Jun 20, 2002 this sequence version replaced gi:17488621.
----- Genome Center
Center: University of Washington Genome Center
Center Code: UWGC
Web site: http://www.genome.washington.edu
Contact: uwgchgs@u.washington.edu
Drafting Center: WUGSC
----- Project Information
Center project name: chr-3
Center clone name: RP11-793E15 (bc0564)
----- Summary Statistics
Sequencing vector: unknown; 52% of reads
Chemistry: Dye-terminator ET; 94% of reads
Chemistry: Dye-terminator Big Dye; 6% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 197168 bases at least Q40
Consensus quality: 197255 bases at least Q30
Consensus quality: 197275 bases at least Q20
Insert size: 197279; sum-of-contigs
Quality coverage: 8.2x in Q20 bases; sum-of-contigs

Overlapping Sequences:
5': RP11-91E8 (UWGC:bc0216) AC026349
3': CTD-2563A18 (UWGC:bc0730)

Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
GenBank flat file format but are available as part
of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:
all regions were either double-stranded or sequenced with an
alternate chemistry or covered by high quality data (i.e., Phred
quality >= 30); an attempt was made to resolve all sequencing
problems, such as compressions and repeats; all regions were
covered by at least one plasmid subclone or more than one M13

subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

HindIII				BglII				EcoRI			
SeqDerMap	FrngPrnt	SeqDerMap	FrngPrnt	SeqDerMap	FrngPrnt	SeqDerMap	FrngPrnt	SeqDerMap	FrngPrnt	SeqDerMap	FrngPrnt
2687	2617	8949	8586	8996	8661						
6382	6410	2067	2160	6	<800						
512	<800	7846	7940	2742	2803						
449	<800	3734	3895	5376	5324						
2602	2763	1334	1301	1493	1478						
2590	2617	2287	2309	823	835						
8313	8291	1814	1918	1962	2002						
1711	1683	691	<800	2900	2954						
9821	9472	5477	5348	1484	1478						
516	<800	305	<800	1005	995						
8587	8291	25245	25541	1181	1171						
7446	7581	3988	4121	18560	19002						
2088	2075	1633	1598	3603	3579						
2509	2617	631	<800	4943	5076						
3519	3501	90	<800	3239	3241						
26	<800	402	<800	953	995						
925	933	3350	3490	1621	1615						
98	<800	4577	4515	6827	6900						
6409	6410	1229	1183	79	<800						
1383	1376	4221	4331	16418	16263						
16048	15829	3980	4121	3361	3241						
1876	1877	2548	2497	872	881						
4169	4068	674	<800	4220	4193						
1674	1683	2332	2309	2848	2803						
52	<800	11445	11045	2283	2318						
5227	5082	5692	5632	3211	3241						
15464	15829	1385	1414	4615	4632						

14333	14296	608	<800	6823	6900
1026	1026	3930	3895	886	881
645	<800	1465	1414	2032	2002
6621	6410	2382	2497	8680	8661
8413	8291	747	<800	5163	5076
1401	1376	1951	2012	1547	1478
1512	1471	642	<800	7058	6900
5801	5644	21060	21003	1647	1615
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3448	3501	1321	1301	162	<800
2738	2763	10705	10502	1078	1093
237	<800	3128	3317	2156	2173
6715	6823	183	<800	5077	5076
201	<800	3255	3490	154	<800
1002	1026	5693	5632	1571	1478
221	<800	3380	3317	219	<800
2854	2899	237	<800	520	<800
6998	7317	431	<800	1540	1478
1174	1145	2152	2160	1479	1478
7876	8291	249	<800	1613	1615
1911	1877	2599	2778	1399	1478
3899	3847	685	<800	9553	9383
5672	5644	41	<800	166	<800
1711	1683	388	<800	13615	13115
862	854	2500	2497	4731	4632
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		178	<800	4503	4430
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Query Match 100.0%; Score 51; DB 9; Length 197279;
 Best Local Similarity 100.0%; Pred. No. 3.6e-09;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTACCACTGGTCTCTTGTGCTTATCCGGGCAAGAACTTATCGAATACA 51
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 Db 167486 GGTACCACTGGTCTCTTGTGCTTATCCGGGCAAGAACTTATCGAATACA 167536

RESULT 10

HSA312688

LOCUS

DEFINITION

SEQUENCING IN PROGRESS ***

220965 bp

DNA

linear

HTG 15-MAY-2002

Homo sapiens chromosome 3 clone RP6-32g23 map 3p21.3, ***

26 ordered pieces.

ACCESSION AJ312688
 VERSION AJ312688.2 GI:13559235
 KEYWORDS HTG: HTGS_PHASE2.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1
 Kiss, H., Yang, Y., Kiss, C., Andersson, K., Klein, G., Imreh, S. and
 Dunanski, J.P.
 TITLE The transcriptional map of the common eliminated region 1 (C3CER1)
 in 3p21.3
 Eur. J. Hum. Genet. 10 (1), 52-61 (2002)
 JOURNAL 21906202
 MEDLINE 11896456
 PUBMED
 REFERENCE 2 (bases 1 to 220965)
 AUTHORS Kiss, H.
 DIRECT SUBMISSION
 SUBMITTED (01-APR-2001) Kiss H., Microbiology and Tumorbiology
 Center (MTC), Karolinska Institute, Box 280, Stockholm, S-17177,
 SWEDEN
 COMMENT On Apr 5, 2001 this sequence version replaced gi:13548633.
 The sequence is a consensus sequence of clone RP4-787c23 (1-140400
 bp),
 clone RP6-32g23 (31212-220965 bp), clone RP6-146e1 (partially,
 1-6800 bp)
 and clone RP6-188g11 (partially, 1-108303 bp). The sequencing
 contigs are
 in order and the gaps between them are represented by 100 Ns.
 Contig 1:
 1-11731 bp Contig 2: 11832-26218 bp Contig 3: 26319-28347 bp
 Contig 4:
 28448-42160 bp Contig 5: 42261-55059 bp Contig 6: 55160-61578 bp
 Contig
 7: 61679-97342 bp Contig 8: 97443-117655 bp Contig 9:
 117756-118727 bp
 Contig 10: 118828-121834 bp Contig 11: 121935-127855 bp Contig
 12:
 127956-129383 bp Contig 13: 129484-131747 bp Contig 14:
 131848-132316 bp
 Contig 15: 132417-134455 bp Contig 16: 134556-135527 bp Contig
 17:
 135628-189051 bp Contig 18: 189152-189476 bp Contig 19:
 189577-191375 bp
 Contig 20: 191476-201473 bp Contig 21: 201574-202307 bp Contig
 22:
 202408-204878 bp Contig 23: 204979-213531 bp Contig 24:
 213632-218109 bp
 Contig 25: 218210-219800 bp Contig 26: 219901-220965 bp.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 26 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * provided by the submitter.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
 * 1 11731: contig of 11731 bp in length
 * 11732 11831: gap of 100 bp
 * 11832 26218: contig of 14387 bp in length
 * 26219 26318: gap of 100 bp
 * 26319 28347: contig of 2029 bp in length
 * 28348 28447: gap of 100 bp
 * 28448 42160: contig of 13713 bp in length
 * 42161 42360: gap of 200 bp
 * 42361 55059: contig of 12699 bp in length
 * 55060 55159: gap of 100 bp
 * 55160 61578: contig of 6419 bp in length
 * 61579 61678: gap of 100 bp
 * 61679 97342: contig of 35664 bp in length
 * 97343 97443: gap of 100 bp
 * 97443 117655: contig of 20213 bp in length

* 117656 117755: gap of 100 bp
 * 117756 118727: contig of 972 bp in length
 * 118728 118827: gap of 100 bp
 * 118828 121834: contig of 3007 bp in length
 * 121835 121934: gap of 100 bp
 * 121935 127855: contig of 5921 bp in length
 * 127856 127955: gap of 100 bp
 * 127956 129383: contig of 1428 bp in length
 * 129384 129484: gap of 100 bp
 * 129484 131748: contig of 2264 bp in length
 * 131748 132316: contig of 469 bp in length
 * 132317 132416: gap of 100 bp
 * 132417 134455: contig of 2039 bp in length
 * 134456 134555: gap of 100 bp
 * 134556 135527: contig of 972 bp in length
 * 135528 135627: gap of 100 bp
 * 135628 189051: contig of 53424 bp in length
 * 189052 189151: gap of 100 bp
 * 189152 189476: contig of 325 bp in length
 * 189477 189576: gap of 100 bp
 * 189577 191375: contig of 1799 bp in length
 * 191376 191475: gap of 100 bp
 * 191476 201473: contig of 998 bp in length
 * 201474 201573: gap of 100 bp
 * 201574 202307: contig of 734 bp in length
 * 202308 204878: contig of 2471 bp in length
 * 204879 204978: gap of 100 bp
 * 204979 213531: contig of 8553 bp in length
 * 213532 213631: gap of 100 bp
 * 213632 218109: contig of 4478 bp in length
 * 218110 218209: gap of 100 bp
 * 218210 219800: contig of 1591 bp in length
 * 219801 219900: gap of 100 bp
 * 219901 220965: contig of 1065 bp in length.
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 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GGTACCACTGGTCTTCTTGCTTATCCGGGCAAGACTTATCGAATACA 51
 Db 121110 GGTACCACTGGTCTTCTTGCTTATCCGGGCAAGACTTATCGAATACA 121160
 RESULT 11
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 LOCUS Homo sapiens CC chemokine receptor 3 (CCR3) gene, promoter region
 DEFINITION and partial sequence.
 AF247359
 ACCESSION AF247359
 VERSION AF247359.1 GI:19110540
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1454)
 REFERENCE Vijn, S., Dayhoff, D.E., Wang, C.E., Imam, Z., Ehrenberg, P.K. and
 Michael, N.L.
 AUTHORS Transcription Regulation of Human Chemokine Receptor CCR3: Evidence
 for a Rare TATA-less Promoter Structure Conserved between
 Drosophila and Humans

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JOURNAL Genomics 80 (1), 86-95 (2002)
MEDLINE 22074933
REFERENCE 12079287
AUTHORS 2 (bases 1 to 1454)
TITLE Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
JOURNAL Direct Submission
SUBMITTED (21-MAR-2000) Dept. of Mol. Diag. and Pathogenesis, U.S.
MILITARY HIV Research Program, 1600 E. Gude Drive, Rockville, MD
20850, USA
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Db 1083 GGTACCACTGGTCTTCTTGTCCTATCCGGGCGAGAACTATCGAAATACA 1133

RESULT 12
AF224495 260 bp mRNA linear PRI 02-MAY-2001
LOCUS Homo sapiens CC chemokine receptor 3 (CCR3) mRNA, partial cds.
DEFINITION AF224495
ACCESSION AF224495
VERSION AF224495.1 GI:13924481
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
    1 (bases 1 to 260)
AUTHORS Scotet,E.J.
TITLE CCR3 expression is associated with chromatin remodeling in Th2
    cells
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 260)
AUTHORS Scotet,E.J.
TITLE Direct Submission
JOURNAL Submitted (13-JAN-2000) Basel Institute for Immunology, 487
    Grenzachstrasse, Basel CH-4005, Switzerland
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    Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ACCACTGGTCTTCTTGTCCTATCCGGGCAAGAACTTATCGAAATACA 51
Db 1 ACCACTGGTCTTCTTGTCCTATCCGGGCAAGAACTTATCGAAATACA 48

RESULT 13
AF262301 406 bp mRNA linear PRI 26-JUN-2002
LOCUS Homo sapiens clone 4 CC chemokine receptor 3 (CCR3) mRNA, partial
DEFINITION AF262301
ACCESSION AF262301
VERSION AF262301.1 GI:19171644
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
    1 (bases 1 to 406)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and
    Michael,N.L.
TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence
    for a Rare ThRA-Less Promoter Structure Conserved between
    Drosophila and Humans
JOURNAL Genomics 80 (1), 86-95 (2002)
MEDLINE 22074933
REFERENCE 12079287
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
TITLE Direct Submission
SUBMITTED (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis,
    Walter Reed Army Institute of Research, 1600 E. Gude Drive,
    Rockville, MD 20850, USA
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    Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ACCACTGGTCTTCTTGTCCTATCCGGGCAAGAACTTATCGAAATACA 51

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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 212)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence for a Rare TATA-less Promoter Structure Conserved between Drosophila and Humans
JOURNAL Genomics 80 (1), 86-95 (2002)
MEDLINE 22074933
PUBMED 12079287
REFERENCE 2 (bases 1 to 212)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
TITLE Direct Submission
JOURNAL Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis, Walter Reed Army Institute of Research, 1600 E. Gude Drive, Rockville, MD 20850, USA
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Db 1 CCACCTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGAATACA 47
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Job time : 1437 secs

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DEFINITION Homo sapiens clone 5 CC chemokine receptor 3 (CCR3) mRNA, partial cds.
ACCESSION AF262302
VERSION AF262302.1 GI:19171646
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 410)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence for a Rare TATA-less Promoter Structure Conserved between Drosophila and Humans
JOURNAL Genomics 80 (1), 86-95 (2002)
MEDLINE 22074933
PUBMED 12079287
REFERENCE 2 (bases 1 to 410)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
TITLE Direct Submission
JOURNAL Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis, Walter Reed Army Institute of Research, 1600 E. Gude Drive, Rockville, MD 20850, USA
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Best Local Similarity 100.0%; Pred. No. 6.8e-08;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 ACCACTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGAATACA 51
Db 1 ACCACTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGAATACA 48
RESULT 15
LOCUS AF262303 212 bp mRNA linear PRI 26-JUN-2002
DEFINITION Homo sapiens clone 6 CC chemokine receptor 3 (CCR3) mRNA, partial cds.
ACCESSION AF262303
VERSION AF262303.1 GI:19171648
KEYWORDS

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)
1934.510 Million cell updates/sec

Title: US-10-068-067-16

Perfect score: 51

Sequence: 1 ggtaccactggtctcttgtt.....caagaacttatcgaaataca 51

Scoring table:

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Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

Database :

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1: gb_ba.*

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13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

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26: em_ro.*

27: em_sts.*

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29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rod.*

36: em_htg_mam.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	51	100.0	51	6	AX513217	AX513217 Sequence
2	51	100.0	51	6	AX513222	AX513222 Sequence
3	51	100.0	348	9	AF262239	AF262239 Homo sapi
4	51	100.0	957	9	AF224496	AF224496 Homo sapi
5	51	100.0	1453	9	AF247360	AF247360 Homo sapi
6	51	100.0	2895	6	AX513212	AX513212 Sequence
7	51	100.0	2895	9	AF237380S1	AF237380 Homo sapi
8	51	100.0	177334	9	AC138069	AC138069 Homo sapi
9	51	100.0	197279	9	AC104439	AC104439 Homo sapi
10	51	100.0	220965	2	HSJ312888	AJ312688 Homo sapi
11	48	94.1	260	9	AF224495	AF224495 Homo sapi
12	48	94.1	406	9	AF262301	AF262301 Homo sapi
13	48	94.1	410	9	AF262302	AF262302 Homo sapi
14	47	92.2	212	9	AF262303	AF262303 Homo sapi
15	47	92.2	436	9	AF262304	AF262304 Homo sapi
16	35	68.6	1193	6	BD082061	BD082061 G-protein
17	35	68.6	1193	6	BD082061	AF247359 Homo sapi
18	32	62.7	1454	9	AF247359	AX513218 Sequence
19	22	43.1	22	6	AX513219	AX513219 Sequence
20	22	43.1	22	6	AX513224	AX513224 Sequence
21	22	43.1	22	6	AX513220	AX513220 Sequence
22	21	41.2	21	6	AX513223	AX513223 Sequence
23	21	41.2	21	6	AX513225	AX513225 Sequence
24	21	41.2	21	6	AX513225	AL669871 Mouse DNA
25	19	37.3	208519	10	AL669871	282260 Caenorhabdi
26	18	35.3	31654	3	CEC32H11	AF041468 Guillard
27	18	35.3	121524	8	AF041468	AC144357 Danio rer
28	18	35.3	173554	2	AC144357	AF180024 Huperzia
29	17	33.3	2145	8	AF180024	X05847 C.reinhardt
30	17	33.3	3187	8	CHCRPS13	L27836 Plasmodium
31	17	33.3	6951	3	PFARHPR	AF323443 Plasmodiu
32	17	33.3	8241	3	AF323443	AF323442 Plasmodiu
33	17	33.3	8256	3	AF323442	AC129517 Homo sapi
34	17	33.3	58883	2	AC129517	282217 Human DNA s
35	17	33.3	73031	9	HS78B3	AL080272 Human DNA
36	17	33.3	95556	9	HSJ73H14	AC020389 Drosophil
37	17	33.3	95613	2	AC020389	AC141177 Rattus no
38	17	33.3	112182	2	AC141177	BX293986 Mouse DNA
39	17	33.3	114458	10	BS293986	AL663002 Oryza sat
40	17	33.3	128574	8	OSJN00199	AL034554 Human DNA
41	17	33.3	137739	9	HS994L9	AF003235 Oryza sat
42	17	33.3	148892	8	AP003235	AC006495 Drosophil
43	17	33.3	155840	2	AC006495	AC083842 Homo sapi
44	17	33.3	161079	2	AC083842	AL358532 Human DNA
45	17	33.3	161826	9	AL358532	

ALIGNMENTS

RESULT 1
AX513217
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

AX513217
Sequence 16 from Patent WO02062848.
AX513217
AX513217.1 GI:23504280
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Rothenberg, M.E. and Zimmerman, N.
Regulation of cc chemokine receptor 3 (ccr3) expression
Patent: WO 02062848-A 16 15-AUG-2002;

AX513217
Sequence 16 from Patent WO02062848.
AX513217
AX513217.1 GI:23504280
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Rothenberg, M.E. and Zimmerman, N.
Regulation of cc chemokine receptor 3 (ccr3) expression
Patent: WO 02062848-A 16 15-AUG-2002;

AX513217
Sequence 16 from Patent WO02062848.
AX513217
AX513217.1 GI:23504280
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Rothenberg, M.E. and Zimmerman, N.
Regulation of cc chemokine receptor 3 (ccr3) expression
Patent: WO 02062848-A 16 15-AUG-2002;

CHILDREN'S HOSPITAL MEDICAL CENTER (US)

FEATURES

source
Location/Qualifiers
1. .51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 51; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 2e-19;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTACCACTGGTCTTCTGTGCTTATCCGGGCAAGAACTTATCGAATACA 51
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Db 1 GGTACCACTGGTCTTCTGTGCTTATCCGGGCAAGAACTTATCGAATACA 51

RESULT 2
AX513222 AX513222 51 bp RNA linear PAT 03-OCT-2002
LOCUS
DEFINITION Sequence 21 from Patent WO02062848.
ACCESSION AX513222
VERSION AX513222.1 GI:23504285

KEYWORDS

source Homo sapiens (human)

ORIGIN

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1

REFERENCE

AUTHORS Rotherberg,M.E. and Zimmerman,N.

TITLE Regulation of cc chemokine receptor 3 (ccr3) expression

JOURNAL Patent: WO 02062848-A 21 15-AUG-2002;

CHILDREN'S HOSPITAL MEDICAL CENTER (US)

FEATURES

source
Location/Qualifiers
1. .51
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 51; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 2e-19;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTACCACTGGTCTTCTGTGCTTATCCGGGCAAGAACTTATCGAATACA 51
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Db 1 GGTACCACTGGTCTTCTGTGCTTATCCGGGCAAGAACTTATCGAATACA 51

RESULT 3
AF262299 AF262299 348 bp mRNA linear PRI 26-JUN-2002
LOCUS
DEFINITION Homo sapiens clone 1 CC chemokine receptor 3 (CCR3) mRNA, partial cds.

ACCESSION

VERSION AF262299.1 GI:19171640

KEYWORDS

source Homo sapiens (human)

ORIGIN

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 348)

Vijh,S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and

Michael,N.L.

Transcription Regulation of Human Chemokine Receptor CCR3: Evidence

for a Rare TATA-less Promoter Structure Conserved between

Drosophila and Humans

Genomics 80 (1), 86-95 (2002)

JOURNAL

MEDLINE 22074933

PUBMED 12079287

REFERENCE

2 (bases 1 to 348)

AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.

TITLE Direct Submission

JOURNAL

Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis,
Walter Reed Army Institute of Research, 1600 E. Gude Drive,
Rockville, MD 20850, USA

FEATURES

source
Location/Qualifiers
1. .348
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

/chromosome="3"

/map="3p21"

/clone="11"

/cell_type="eosinophil"

1. .348

/gene="CCR3"

120. .348

/gene="CCR3"

/note="G-protein coupled receptor; principal eotaxin
receptor expressed on eosinophils, CD4 Th2 lymphocytes,
CD8 lymphocytes, microglia, dendritic cells, and
monocytes"

/codon_start=1

/product="CC chemokine receptor 3"

/protein_id="AAL85628.1"

/db_xref="GI:19171641"

/translation="MTSLDTVEFTGTSYDDVGLLCEKADTRALMAQVFPLYSLV

FTVGLGNVVVMILIKIRLRIMNIYLLNL"

ORIGIN

Query Match 100.0%; Score 51; DB 9; Length 348;
Best Local Similarity 100.0%; Pred. No. 1.9e-19;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTACCACTGGTCTTCTGTGCTTATCCGGGCAAGAACTTATCGAATACA 51

|||||

Db 27 GGTACCACTGGTCTTCTGTGCTTATCCGGGCAAGAACTTATCGAATACA 77

RESULT 4

AF224496S1

LOCUS

DEFINITION Homo sapiens CC chemokine receptor 3 (CCR3) gene, exon 1.

ACCESSION AF224496

VERSION AF224496.1 GI:13924485

KEYWORDS

1 of 2

SEGMENT

SOURCE Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 957)

AUTHORS Scotet,E.J.

TITLE CCR3 expression is associated with chromatin remodeling in Th2

cells

JOURNAL Unpublished

REFERENCE

2 (bases 1 to 957)

AUTHORS Scotet,E.J.

TITLE Direct Submission

JOURNAL Submitted (13-JAN-2000) Basel Institute for Immunology, 487

Grenzacherstrasse, Basel CH-4005, Switzerland

FEATURES

source

Location/Qualifiers

1. .957

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

298. .376

/gene="CCR3"

/note="exon 1"

ORIGIN

Query Match 100.0%; Score 51; DB 9; Length 957;

Best Local Similarity 100.0%; Pred. No. 1.9e-19;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACCACTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGAAATACA 51
 |||||||
 Db 295 GGTACCACTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGAAATACA 345
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RESULT 5
 AF247360 1453 bp DNA linear PRI 26-JUN-2002
 LOCUS Homo sapiens CC chemokine receptor 3 (CCR3) gene, promoter region
 DEFINITION and partial sequence.
 ACCESSION AF247360
 VERSION AF247360.1 GI:191110541
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1453)
 AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and Michael,N.L.
 TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence for a Rare TATA-less Promoter Structure Conserved between Drosophila and Humans
 JOURNAL Genomics 80 (1), 86-95 (2002)
 MEDLINE 22074933
 PUBMED 12079287
 REFERENCE 2 (bases 1 to 1453)
 AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
 TITLE Direct Submission
 JOURNAL Submitted (21-MAR-2000) Dept. of Mol. Diag. and Pathogenesis, U.S. Military HIV Research Program, 1600 E. Gude Drive, Rockville, MD 20850, USA

FEATURES
 source
 1. 1453
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="3"
 /map="3p21; between CCR1 and CCR5"
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 /cell_type="peripheral blood mononuclear cell"
 1..1453
 /gene="CCR3"
 755
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 822..>1453
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 822..1163
 /gene="CCR3"
 1114
 /gene="CCR3"
 /replace="g"

ORIGIN
 Query Match 100.0%; Score 51; DB 9; Length 1453;
 Best Local Similarity 100.0%; Pred. No. 1.8e-19;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACCACTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGAAATACA 51
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 Db 1082 GGTACCACTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGAAATACA 1132
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RESULT 6
 AX513212 2895 bp DNA linear PAT 03-OCT-2002
 LOCUS Sequence 11 from Patent WO02062848.
 DEFINITION
 ACCESSION AX513212
 VERSION AX513212.1 GI:23504275
 KEYWORDS
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Rothenberg,M.E. and Zimmerman,N.
 TITLE Regulation of cc chemokine receptor 3 (ccr3) expression
 JOURNAL Patent: WO 02062848-A 11 15-AUG-2002;
 CHILDREN'S HOSPITAL MEDICAL CENTER (US)
 FEATURES
 source
 1. 2895
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 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 1.8e-19;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACCACTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGAAATACA 51
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 Db 1561 GGTACCACTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGAAATACA 1611
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RESULT 7
 AF237380S1 2895 bp DNA linear PRI 05-OCT-2000
 LOCUS Homo sapiens CCR3 gene, promoter and exon 1.
 DEFINITION
 ACCESSION AF237380
 VERSION AF237380.1 GI:10643652
 KEYWORDS
 SEGMENT
 SOURCE 1 of 2
 ORGANISM Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 2895)
 AUTHORS Zimmerman,N., Daugherty,B.L., Kavanaugh,J.L., El-Awar,F.Y., Moulton,E.A. and Rothenberg,M.E.
 TITLE Analysis of the CC chemokine receptor 3 gene reveals a complex 5' exon organization, a functional role for untranslated exon 1, and a broadly active promoter with eosinophil-selective elements
 JOURNAL Blood 96 (7), 2346-2354 (2000)
 MEDLINE 20458773
 PUBMED 11001881
 REFERENCE 2 (bases 1 to 2895)
 AUTHORS Daugherty,B.L.
 TITLE Direct Submission
 JOURNAL Submitted (22-FEB-2000) Immunology & Rheumatology, Merck Research Laboratories, 126 East Lincoln Avenue, Rahway, NJ 07065, USA

FEATURES
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 1. 2895
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 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
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 /map="3p21"
 /clone="350-3B"
 /clone_lib="BglII fragment from phage P1 human genomic library (DMPC-HFF No. 1; Genome Systems, Inc., St. Louis, MO)"
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 /gene="CCR3"
 33..38
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 1287..1292
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 1552..1642
 /gene="CCR3"
 /note="untranslated"
 /number=1

ORIGIN
 promoter
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 /gene="CCR3"
 CAAT_signal
 33..38
 /gene="CCR3"
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Query Match 100.0%; Score 51; DB 9; Length 2895;
 Best Local Similarity 100.0%; Pred. NO. 1.8e-19;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGTACCACTGGTCTTCTTGCTATCCGGCGAGAACTTATCGAATACA 51
 Db 1561 GGTACCACTGGTCTTCTTGCTATCCGGCGAGAACTTATCGAATACA 1611

RESULT 8

AC138069 177334 bp DNA linear PRI 19-FEB-2003
 LOCUS Homo sapiens chromosome 3 clone RP13-54612, complete sequence.

AC138069
 ACCESSION AC138069.3 GI:28416170
 VERSION
 KEYWORDS
 SOURCE

ORGANISM Homo sapiens (human)

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
 Saenphimmachak,C., Buckley,D., Kibukawa,M., Raymond,C. and
 Haugen,E.D.

TITLE Direct Submission

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 177334)
 Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.

TITLE Direct Submission

JOURNAL Submitted (12-DEC-2002) Genome Center, University of Washington,
 Box 352145, Seattle, WA 98195, USA

REFERENCE 3 (bases 1 to 177334)
 Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.

TITLE Direct Submission

JOURNAL Submitted (10-JAN-2003) Genome Center, University of Washington,
 Box 352145, Seattle, WA 98195, USA

REFERENCE 4 (bases 1 to 177334)
 Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
 Saenphimmachak,C., Buckley,D., Kibukawa,M., Raymond,C. and
 Haugen,E.D.

TITLE Direct Submission

JOURNAL Submitted (19-FEB-2003) Genome Center, University of Washington,
 Box 352145, Seattle, WA 98195, USA

COMMENT On Feb 19, 2003 this sequence version replaced gi:27573398.

Center: University of Washington Genome Center

Center Code: UWGC

Web site: <http://www.genome.washington.edu>

Contact: uwgchgs@u.washington.edu

Center project name: chr-3

Center clone name: RP13-54612 (bc0820)

Sequencing vector: plasmid; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 177210 bases at least Q40

Consensus quality: 177313 bases at least Q30

Consensus quality: 177334 bases at least Q20

Insert size: 177334; sum-of-contigs

Quality coverage: 9.3x in Q20 bases; sum-of-contigs

Overlapping Sequences:

5': RP11-793E15 (UWGC:bc0564) AC104439, 95469-bp overlap

3': U95626, 42710-bp overlap

Sequence Quality Assessment:

This entry has been annotated with sequence quality

estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality zero.

Quality levels above 40 are expected to have less than

1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the

GenBank flat file format but are available as part
 of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:
 all regions were either double-stranded or sequenced with an
 alternate chemistry or covered by high quality data (i.e., Phred
 quality >= 30); an attempt was made to resolve all sequencing
 problems, such as compressions and repeats; all regions were
 covered by at least one plasmid subclone or more than one M13
 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest
 fingerprinting. Comparison of the experimentally derived digest
 fragments with sequence-predicted fragments is given below.

The electronically-digested sequence consists of both insert and
 vector, in order to accurately represent the entire circular BAC.

Small fragments below a variable cutoff (approximately 400-800 bp)
 are not resolved in the fingerprint and hence do not appear

in the table. There are no significant remaining discrepancies
 between the experimental and predicted values. Uniquely ordered

fragments are separated by dashed lines.

HindIII EcoRI BglII

SeqDerMap	FrgrPrnt	SeqDerMap	FrgrPrnt	SeqDerMap	FrgrPrnt
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1239	1199	11125	10952	6306	6319
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449	<800	2290	2310	2067	2071
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510	<800	560	<800	3913	3756
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6511	6363	54	<800	2169	2210
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5296	5509	1159	1158	910	910
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10424	10027	4052	4034	875	893
-----	-----	-----	-----	-----	-----
5046	5119	1846	1829	3716	3756
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1196	1199	8334	8273	4502	4523
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1397	1392	12882	12573	1967	1945
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2597	2624	448	<800	2864	2871
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1688	1674	12737	12573	4724	4738
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3800	3818	10300	10103	4773	4738
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2248	2269	6671	6656	3707	3756
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1074	1055	4052	4034	336	<800
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7303	7718	1392	1386	79	<800
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959	959	4253	4286	4736	4738
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551	<800	2791	2834	1859	1945
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1074	1055	2647	2682	3696	3756
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5688	5759	3423	3409	1569	1539
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5183	5363	73	<800	8078	8038
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3100	3093	499	<800	1365	1325
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921	959	723	<800	289	<800
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4350	4244	2763	2834	11047	10790

4931	4857	6594	6656	8848	8963
3907	3818	4503	4468	1914	1945
8001	7718	5154	5136	1336	1325
3804	3818	4730	4713	11485	11341
2355	2376	13628	13324	974	975
862	868	166	<800	2448	2501
1711	1674	9554	9494	373	<800
5672	5759	1398	1386	1003	975
3900	3818	1613	1641	1787	1756
1905	1854	1479	1503	857	883
7872	7718	1540	1503	1974	1945
1174	1155	520	<800	1707	1631
7015	7139	219	<800	3835	3756
2852	2868	1571	1503	6586	6551
221	<800	154	<800	178	<800
1002	1055	5077	5136	2905	2871
201	<800	2156	2190	2500	2501
6717	6864	1075	1089	389	<800
237	<800	162	<800	41	<800
2737	2749	2752	2834	685	<800
3448	3416	1647	1641	2598	2662
3256	3238	7059	7056	248	<800
5801	5759	1547	1503	2152	2210
1512	1497	5163	5136	431	<800
1398	1392	8679	8719	237	<800
8413	8333	2033	2035	3380	3411
6621	6614	886	892	5694	5744
645	<800	---	3255	3255	3265
1026	1055	---	183	183	<800
14333	14484	---	3128	3128	3144
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Query Match 100.0%; Score 51; DB 9; Length 177334;

Best Local Similarity 100.0%; Pred. No. 1.6e-19;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACACTGGTCTTCTTGTGCTTATCCGGGCAAGAACTTATCGAAATACA 51

DB 65693 GGTACCACTGGTCTTCTTGTGCTTATCCGGGCAAGAACTTATCGAAATACA 65743

RESULT 9
AC104439
LOCUS
DEFINITION
AC104439 AC024739
AC104439.2 GI:21490240
HIG.
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 197279)
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.
and Haugen, E.D.
Direct Submission
Unpublished
2 (bases 1 to 197279)
Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.
Direct Submission
Submitted (11-DEC-2001) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
3 (bases 1 to 197279)
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.
and Haugen, E.D.
Direct Submission
Submitted (20-JUN-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
On Jun 20, 2002 this sequence version replaced gi:17488621.
----- Genome Center
Center: University of Washington Genome Center
Center Code: UWGC
Web site: <http://www.genome.washington.edu>
Contact: uwgctg@u.washington.edu
Drafting Center: WUGSC
----- Project Information
Center project name: Chr-3
Center clone name: RP11-793E15 (bc0564)
----- Summary Statistics
Sequencing vector: unknown; 52% of reads
Sequencing method: plasmid; 108752; 48% of reads
Chemistry: Dye-terminator ET; 94% of reads
Chemistry: Dye-terminator Big Dye; 6% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 197168 bases at least Q40
Consensus quality: 197255 bases at least Q30
Consensus quality: 197275 bases at least Q20
Insert size: 197279; sum-of-contigs
Quality coverage: 8.2x in Q20 bases; sum-of-contigs

Overlapping Sequences:
5': RP11-51E8 (UWGC:bc0216) AC026349
3': CTD-2563A18 (UWGC:bc0730)

Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
Genbank flat file format but are available as part
of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:
all regions were either double-stranded or sequenced with an
alternate chemistry or covered by high quality data (i.e., Phred
quality >= 30); an attempt was made to resolve all sequencing
problems, such as compressions and repeats; all regions were
covered by at least one plasmid subclone or more than one M13

subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

HindIII				BglII				EcoRI			
SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt
2687	2617	8949	8586	8996	8661	8996	8661	8996	8661	8996	8661
6382	6410	2067	2160	6	<800	6	<800	6	<800	6	<800
512	<800	7846	7940	2742	2803	2742	2803	2742	2803	2742	2803
449	<800	3734	3895	5376	5324	5376	5324	5376	5324	5376	5324
2602	2763	1334	1301	1493	1478	1493	1478	1493	1478	1493	1478
2590	2617	2287	2309	823	835	823	835	823	835	823	835
8313	8291	1814	1918	1962	2002	1962	2002	1962	2002	1962	2002
1711	1683	691	<800	2900	2954	2900	2954	2900	2954	2900	2954
9821	9472	5477	5348	1484	1478	1484	1478	1484	1478	1484	1478
516	<800	305	<800	1005	995	1005	995	1005	995	1005	995
8587	8291	25245	25541	1181	1171	1181	1171	1181	1171	1181	1171
7446	7581	3988	4121	18560	19002	18560	19002	18560	19002	18560	19002
2088	2075	1633	1598	3603	3579	3603	3579	3603	3579	3603	3579
2509	2617	631	<800	4943	5076	4943	5076	4943	5076	4943	5076
3519	3501	90	<800	3239	3241	3239	3241	3239	3241	3239	3241
26	<800	402	<800	953	995	953	995	953	995	953	995
925	933	3350	3490	1621	1615	1621	1615	1621	1615	1621	1615
98	<800	4577	4515	6827	6900	6827	6900	6827	6900	6827	6900
6409	6410	1229	1183	79	<800	79	<800	79	<800	79	<800
1383	1376	4221	4331	16418	16263	16418	16263	16418	16263	16418	16263
16048	15829	3980	4121	3361	3241	3361	3241	3361	3241	3361	3241
1876	1877	2548	2497	872	881	872	881	872	881	872	881
4169	4068	674	<800	4220	4193	4220	4193	4220	4193	4220	4193
1674	1683	2332	2309	2848	2803	2848	2803	2848	2803	2848	2803
52	<800	11445	11045	2283	2318	2283	2318	2283	2318	2283	2318
5227	5082	5692	5632	3211	3241	3211	3241	3211	3241	3211	3241
15464	15829	1385	1414	4615	4632	4615	4632	4615	4632	4615	4632

14333	14296	608	<800	6823	6900
1026	1026	3930	3895	886	881
645	<800	1465	1414	2032	2002
6621	6410	2382	2497	8680	8661
8413	8291	747	<800	5163	5076
1401	1376	1951	2012	1547	1478
1512	1471	642	<800	7058	6900
5801	5644	21060	21003	1647	1615
3256	3278	3700	3666	2753	2803
3448	3501	1321	1301	162	<800
2738	2763	10705	10502	1078	1093
237	<800	3128	3317	2156	2173
6715	6823	183	<800	5077	5076
201	<800	3255	3490	154	<800
1002	1026	5693	5632	1571	1478
221	<800	3380	3317	219	<800
2854	2899	237	<800	520	<800
6998	7317	431	<800	1540	1478
1174	1145	2152	2160	1479	1478
7876	8291	249	<800	1613	1615
1911	1877	2599	2778	1399	1478
3899	3847	685	<800	9553	9383
5672	5644	41	<800	166	<800
1711	1683	388	<800	13615	13115
862	854	2500	2497	4731	4632
2368	2389	2889	2778	5159	5076
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		6589	6728	6607	6900
		3836	3895	2766	2803

Query Match 100.0%; Score 51; DB 9; Length 197279;
 Best Local Similarity 100.0%; Pred. No. 1.6e-19;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACCACTGGTCTTCTTGCTTATCCGGCAAGAACTTATCGAATACA 51
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 Db 167486 GGTACCACTGGTCTTCTTGCTTATCCGGCAAGAACTTATCGAATACA 167536

RESULT 10
 HSA312688 220965 bp DNA linear HTG 15-MAY-2002
 LOCUS Homo sapiens chromosome 3 clone RP6-32g23 map 3p21.3, ***
 DEFINITION SEQUENCING IN PROGRESS ***, 26 ordered pieces.

ACCESSION AJ312688
VERSION AJ312688.2 GI:13559235
KEYWORDS HTG; HTGS_PHASE2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Kiss, H., Yang, Y., Kiss, C., Andersson, K., Klein, G., Inreh, S. and
Dumanski, J.P.
TITLE The transcriptional map of the common eliminated region 1 (C3CER1)
in 3p21.3
JOURNAL Eur. J. Hum. Genet. 10 (1), 52-61 (2002)
MEDLINE 21906202
PUBMED 11896456
REFERENCE 2 (bases 1 to 220965)
AUTHORS Kiss, H.
TITLE Direct Submission
JOURNAL Submitted (01-APR-2001) Kiss H., Microbiology and Tumorbiology
Center (MTC), Karolinska Institute, Box 280, Stockholm, S-17177,
SWEDEN
COMMENT On Apr 5, 2001 this sequence version replaced gi:13548633.
The sequence is a consensus sequence of clone RP4-787c23 (1-140400
bp),
clone RP6-32g23 (31212-220965 bp), clone RP6-146el (partially,
1-6800 bp)
and clone RP6-188g11 (partially, 1-108303 bp). The sequencing
contigs are
in order and the gaps between them are represented by 100 Ns.
Contig 1:
1-11731 bp Contig 2: 11832-26218 bp Contig 3: 26319-28347 bp
Contig 4:
28448-42160 bp Contig 5: 42261-55059 bp Contig 6: 55160-61578 bp
Contig
7: 61679-97342 bp Contig 8: 97443-117655 bp Contig 9:
117756-118727 bp
Contig 10: 118828-121834 bp Contig 11: 121935-127855 bp Contig
12:
127956-129383 bp Contig 13: 129484-131747 bp Contig 14:
131848-132316 bp
Contig 15: 132417-134455 bp Contig 16: 134556-135527 bp Contig
17:
135628-189051 bp Contig 18: 189152-189476 bp Contig 19:
189577-194375 bp
Contig 20: 191476-201473 bp Contig 21: 201574-202307 bp Contig
22:
202408-204878 bp Contig 23: 204979-213531 bp Contig 24:
213632-218109 bp
Contig 25: 218210-219800 bp Contig 26: 219901-220965 bp.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 26 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 11731: contig of 11731 bp in length
* 11732 11831: gap of 100 bp
* 11832 26218: contig of 14387 bp in length
* 26219 26318: gap of 100 bp
* 26319 28347: contig of 2029 bp in length
* 28348 28448: gap of 100 bp
* 28448 42160: contig of 13713 bp in length
* 42161 42360: gap of 200 bp
* 42361 55059: contig of 12699 bp in length
* 55060 55159: gap of 100 bp
* 55160 61578: contig of 6419 bp in length
* 61579 61679: gap of 100 bp
* 61679 97342: contig of 35664 bp in length
* 97343 97443: gap of 100 bp
* 97443 117655: contig of 20213 bp in length

* 117656 117755: gap of 100 bp
* 117756 118727: contig of 972 bp in length
* 118728 118827: gap of 100 bp
* 118828 121834: contig of 3007 bp in length
* 121835 121934: gap of 100 bp
* 121935 127855: contig of 5921 bp in length
* 127856 127955: gap of 100 bp
* 127956 129383: contig of 1428 bp in length
* 129384 129483: gap of 100 bp
* 129484 131747: contig of 2264 bp in length
* 131748 131847: gap of 100 bp
* 131848 132316: contig of 469 bp in length
* 132317 132416: gap of 100 bp
* 132417 134455: contig of 2039 bp in length
* 134456 134555: gap of 100 bp
* 134556 135527: contig of 972 bp in length
* 135528 135627: gap of 100 bp
* 135628 189051: contig of 53424 bp in length
* 189052 189151: gap of 100 bp
* 189152 189476: contig of 325 bp in length
* 189477 189576: gap of 100 bp
* 189577 191375: contig of 1799 bp in length
* 191376 191475: gap of 100 bp
* 191476 201573: contig of 9998 bp in length
* 201574 202307: contig of 734 bp in length
* 202308 202407: gap of 100 bp
* 202408 204878: contig of 2471 bp in length
* 204879 204979: gap of 100 bp
* 204979 213531: contig of 8553 bp in length
* 213532 213631: gap of 100 bp
* 213632 218109: contig of 4478 bp in length
* 218110 218209: gap of 100 bp
* 218210 219800: contig of 1591 bp in length
* 219801 219900: gap of 100 bp
* 219901 220965: contig of 1065 bp in length.
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/mol_type="genomic DNA"
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Best Local Similarity 100.0%; Pred No. 1.6e-19; Mismatches 0; Indels 0; Gaps 0;
Matches 51; Conservative 0;
Qy 1 GGTACCACTGGTCTTCTTGTGCTTATCCGGGCAAGAACTTATCGAAATACA 51
Db 121110 GGTACCACTGGTCTTCTTGTGCTTATCCGGGCAAGAACTTATCGAAATACA 121160
RESULT 11
AF224495 260 bp mRNA linear PRI 02-MAY-2001
LOCUS Homo sapiens CC chemokine receptor 3 (CCR3) mRNA, partial cds.
DEFINITION AF224495
ACCESSION AF224495
VERSION AF224495.1 GI:13924481
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 260)
AUTHORS Scotet, E.J.
TITLE CCR3 expression is associated with chromatin remodeling in Th2
cells
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 260)
AUTHORS Scotet, E.J.

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TITLE      Direct Submission
JOURNAL    Submitted (13-JAN-2000) Basel Institute for Immunology, 487
           Grenzacherstrasse, Basel CH-4005, Switzerland
FEATURES   source
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             /organism="Homo sapiens"
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           91..>260
             /gene="CCR3"
           /codon_start=1
           /product="CC chemokine receptor 3"
           /protein_id="AAK49027.1"
           /db_xref="GI:13924482"
           /translation="MTTSLDTVETFGTTSYDDVGLLCEKADTRALMAQFVPPLYSLV
           FTVGLLGNVVVV"

ORIGIN
Query Match      94.1%; Score 48; DB 9; Length 260;
Best Local Similarity 100.0%; Pred. No. 1.2e-17;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4  ACCACTGCTCTTCTTGCTTATCCGGGCAAGAACTTATCGAATAACA 51
Db      1  ACCACTGCTCTTCTTGCTTATCCGGGCAAGAACTTATCGAATAACA 48

RESULT 12
LOCUS    AF262301              406 bp      mRNA      linear      PRI 26-JUN-2002
DEFINITION Homo sapiens clone 4 CC chemokine receptor 3 (CCR3) mRNA, partial cds.
ACCESSION AF262301
VERSION   AF262301.1 GI:19171644
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 406)
AUTHORS   Vijh,S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and
           Michael,N.L.
TITLE      Transcription Regulation of Human Chemokine Receptor CCR3: Evidence
           for a Rare TATA-less Promoter Structure Conserved Between
           Drosophila and Humans
JOURNAL   Genomics 80 (1), 86-95 (2002)
MEDLINE   22074933
PUBMED    12079287
REFERENCE 2 (bases 1 to 406)
AUTHORS   Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
TITLE      Direct Submission
JOURNAL   Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis,
           Walter Reed Army Institute of Research, 1600 E. Gude Drive,
           Rockville, MD 20850, USA
FEATURES   Location/Qualifiers
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             /clone="4"
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           CD8 lymphocytes, microglia, dendritic cells, and
           monocytes"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.2e-17;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4  ACCACTGCTCTTCTTGCTTATCCGGGCAAGAACTTATCGAATAACA 51
Db      1  ACCACTGCTCTTCTTGCTTATCCGGGCAAGAACTTATCGAATAACA 48

RESULT 13
LOCUS    AF262302              410 bp      mRNA      linear      PRI 26-JUN-2002
DEFINITION Homo sapiens clone 5 CC chemokine receptor 3 (CCR3) mRNA, partial cds.
ACCESSION AF262302
VERSION   AF262302.1 GI:19171646
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 410)
AUTHORS   Vijh,S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and
           Michael,N.L.
TITLE      Transcription Regulation of Human Chemokine Receptor CCR3: Evidence
           for a Rare TATA-less Promoter Structure Conserved Between
           Drosophila and Humans
JOURNAL   Genomics 80 (1), 86-95 (2002)
MEDLINE   22074933
PUBMED    12079287
REFERENCE 2 (bases 1 to 410)
AUTHORS   Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
TITLE      Direct Submission
JOURNAL   Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis,
           Walter Reed Army Institute of Research, 1600 E. Gude Drive,
           Rockville, MD 20850, USA
FEATURES   Location/Qualifiers
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             /map="3p21"
             /clone="5"
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           monocytes"
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           /product="CC chemokine receptor 3"
           /protein_id="AAL85631.1"
           /db_xref="GI:19171647"
           /translation="MTTSLDTVETFGTTSYDDVGLLCEKADTRALMAQFVPPLYSLV
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ORIGIN
Query Match      94.1%; Score 48; DB 9; Length 410;
Best Local Similarity 100.0%; Pred. No. 1.2e-17;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 4 ACCACTGGTCTTCTTGCTTATCCGGGCAAGAAGAACTTATCGAATACA 51
Db 1 ACCACTGGTCTTCTTGCTTATCCGGGCAAGAAGAACTTATCGAATACA 48

RESULT 14
AF262303
LOCUS
DEFINITION Homo sapiens clone 6 CC chemokine receptor 3 (CCR3) mRNA, partial
cDS.
ACCESSION AF262303
VERSION AF262303.1 GI:19171648
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 212)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and
Michael,N.L.
TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence
for a Rare TATA-less Promoter Structure Conserved between
Drosophila and Humans
Genomics 80 (1), 86-95 (2002)
JOURNAL MEDLINE
PUBMED 12079287
REFERENCE 2 (bases 1 to 212)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
TITLE Direct Submission
Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis,
Walter Reed Army Institute of Research, 1600 E. Gude Drive,
Rockville, MD 20850, USA
JOURNAL Location/Qualifiers
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/feature="CCR3"
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receptor expressed on eosinophils, CD4 Th2 lymphocytes,
CD8 lymphocytes, microglia, dendritic cells, and
monocytes"
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/protein_id="AA05632.1"
/db_xref="GI:19171649"
/translation="MTTSLDTVETFGTTSYYDDVG"

ORIGIN
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Best Local Similarity 100.0%; Pred.No. 4.8e-17;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACGTGGTCTTCTTGCTTATCCGGGCAAGAAGAACTTATCGAATACA 51
Db 1 CCACGTGGTCTTCTTGCTTATCCGGGCAAGAAGAACTTATCGAATACA 47

RESULT 15
AF262304
LOCUS
DEFINITION Homo sapiens clone 7 CC chemokine receptor 3-like mRNA, partial
sequence, alternatively spliced.
ACCESSION AF262304
VERSION AF262304.1 GI:19171650
KEYWORDS
SOURCE Homo sapiens (human)
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 436)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and
Michael,N.L.
TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence
for a Rare TATA-less Promoter Structure Conserved between
Drosophila and Humans
Genomics 80 (1), 86-95 (2002)
JOURNAL MEDLINE
PUBMED 12079287
REFERENCE 2 (bases 1 to 436)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
TITLE Direct Submission
Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis,
Walter Reed Army Institute of Research, 1600 E. Gude Drive,
Rockville, MD 20850, USA
JOURNAL Location/Qualifiers
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1..436
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/note="CC chemokine receptor 3-like; contains exon 1, exon
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Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACGTGGTCTTCTTGCTTATCCGGGCAAGAAGAACTTATCGAATACA 51
Db 1 CCACGTGGTCTTCTTGCTTATCCGGGCAAGAAGAACTTATCGAATACA 47

Search completed: August 2, 2004, 19:07:50
Job time : 1146.66 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 19:08:00 ; Search time 258.078 Seconds

(without alignments)

968.934 Million cell updates/sec

Title: US-10-068-067-16

Perfect score: 51

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Gapop 60.0 , Gapext 60.0

Searched: 3222919 seqs, 2451570024 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6445838

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:

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- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq*

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SUMMARIES

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6	22	43.1	22	14	US-10-068-067-18
7	22	43.1	22	14	US-10-068-067-23
8	21	41.2	21	14	US-10-068-067-19
9	21	41.2	21	14	US-10-068-067-22
10	21	41.2	21	14	US-10-068-067-24
11	17	33.3	11124	14	US-10-108-605-286
12	17	33.3	11184	14	US-10-108-605-284
13	16	31.4	21	16	US-10-349-143-9067
14	16	31.4	265	9	US-09-983-965-904

15	31.4	465	17	US-10-437-963-67946	Sequence 67946, A
16	31.4	586	9	US-09-864-761-12607	Sequence 12607, A
17	31.4	1179	17	US-10-437-963-67946	Sequence 67946, A
18	31.4	1251	15	US-10-198-846-13243	Sequence 13243, A
19	31.4	1761	17	US-10-437-963-67946	Sequence 67946, A
20	31.4	1967	17	US-10-437-963-67946	Sequence 67946, A
21	31.4	3153	13	US-10-282-122A-41935	Sequence 41935, A
22	29.4	234	9	US-09-796-692-2584	Sequence 2584, Ap
23	29.4	234	15	US-10-040-862-2584	Sequence 2584, Ap
24	29.4	234	16	US-10-057-475B-2584	Sequence 2584, Ap
25	29.4	234	16	US-10-154-894B-2584	Sequence 2584, Ap
26	29.4	407	10	US-09-814-353-18713	Sequence 18713, A
27	29.4	423	10	US-09-814-353-21865	Sequence 21865, A
28	29.4	489	9	US-09-070-927A-977	Sequence 977, App
29	29.4	537	10	US-09-991-936-1052	Sequence 1052, Ap
30	29.4	695	13	US-10-027-632-114054	Sequence 114054, A
31	29.4	695	13	US-10-027-632-114055	Sequence 114055, A
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45	29.4	767	16	US-10-027-632-145340	Sequence 145340, A

ALIGNMENTS

RESULT 1
US-10-068-067-16
; Sequence 16, Application US/10068067
; Publication No. US20020151064A1
; GENERAL INFORMATION:
; APPLICANT: Rothenberg, Marc E.
; APPLICANT: Zimmermann, Nives
; APPLICANT: Children's Hospital Medical Center
; TITLE OF INVENTION: REGULATION OF CCR3 EXPRESSION
; FILE REFERENCE: CMC-153
; CURRENT APPLICATION NUMBER: US/10/068,067
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 60/267,073
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-068-067-16

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US-10-068-067-21
; Sequence 21, Application US/10068067
; Publication No. US20020151064A1
; GENERAL INFORMATION:
; APPLICANT: Rothenberg, Marc E.

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; APPLICANT: Zimmermann, Nives
; APPLICANT: Children's Hospital Medical Center
; TITLE OF INVENTION: REGULATION OF CCR3 EXPRESSION
; FILE REFERENCE: CMC-153
; CURRENT APPLICATION NUMBER: US/10/068,067
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 60/267,073
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 51
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-068-067-21

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Matches 36; Conservative 15; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 11, Application US/10068067
; Publication No. US20020151064A1
; GENERAL INFORMATION:
; APPLICANT: Rothenberg, Marc E.
; APPLICANT: Zimmermann, Nives
; APPLICANT: Children's Hospital Medical Center
; TITLE OF INVENTION: REGULATION OF CCR3 EXPRESSION
; FILE REFERENCE: CMC-153
; CURRENT APPLICATION NUMBER: US/10/068,067
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 60/267,073
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 2895
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-068-067-11

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Best Local Similarity 100.0%; Pred. No. 2.5e-20;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACCACTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGAAATACA 51
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RESULT 4
US-10-283-028-3
; Sequence 3, Application US/10283028
; Publication No. US20030143684A1
; GENERAL INFORMATION:
; APPLICANT: Getard, Craig J.
; APPLICANT: Gerard, No. US20030143684A1a P.
; APPLICANT: Mackay, Charles R.
; APPLICANT: Ponath, Paul D.
; APPLICANT: Post, Theodore W.
; APPLICANT: Qin, Shixin
; TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTOR GENE CCR3 AND
; ANTAGONISTS THEREOF
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
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; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; APPLICATION NUMBER: US/10/283,028
; FILING DATE: 28-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/720,565
; FILING DATE: 30-SEP-1996
; APPLICATION NUMBER: PCT/US96/00608
; FILING DATE: 19-JAN-1996
; APPLICATION NUMBER: US 08/375,199
; FILING DATE: 19-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: LKS94-05A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1193 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 92..1156
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-283-028-3

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; Publication No. US20020151064A1
; GENERAL INFORMATION:
; APPLICANT: Rothenberg, Marc E.
; APPLICANT: Zimmermann, Nives
; APPLICANT: Children's Hospital Medical Center
; TITLE OF INVENTION: REGULATION OF CCR3 EXPRESSION
; FILE REFERENCE: CMC-153
; CURRENT APPLICATION NUMBER: US/10/068,067
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 60/267,073
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-068-067-17

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RESULT 6
US-10-068-067-18
; Sequence 18, Application US/10068067
; Publication No. US20020151064A1
; GENERAL INFORMATION:
; APPLICANT: Rothenberg, Marc E.
; APPLICANT: Zimmermann, Nives
; TITLE OF INVENTION: REGULATION OF CCR3 EXPRESSION
; FILE REFERENCE: CMC-153
; CURRENT APPLICATION NUMBER: US/10/068,067
; CURRENT FILING DATE: 2002-02-05
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-068-067-18

Query Match 43.1%; Score 22; DB 14; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CTTGTGCTTATCCGGCGAAGAA 37
DB 1 CTTGTGCTTATCCGGCGAAGAA 22

RESULT 7
US-10-068-067-23
; Sequence 23, Application US/10068067
; Publication No. US20020151064A1
; GENERAL INFORMATION:
; APPLICANT: Rothenberg, Marc E.
; APPLICANT: Zimmermann, Nives
; TITLE OF INVENTION: REGULATION OF CCR3 EXPRESSION
; FILE REFERENCE: CMC-153
; CURRENT APPLICATION NUMBER: US/10/068,067
; CURRENT FILING DATE: 2002-02-05
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-068-067-23

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Best Local Similarity 72.7%; Pred. No. 0.0046;
Matches 16; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CUUGUGCUUACUGCGGCAAGAA 22

RESULT 8
US-10-068-067-19
; Sequence 19, Application US/10068067
; Publication No. US20020151064A1
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; GENERAL INFORMATION:
; APPLICANT: Rothenberg, Marc E.
; APPLICANT: Zimmermann, Nives
; TITLE OF INVENTION: REGULATION OF CCR3 EXPRESSION
; FILE REFERENCE: CMC-153
; CURRENT APPLICATION NUMBER: US/10/068,067
; CURRENT FILING DATE: 2002-02-05
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-068-067-19

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DB 1 GCAAGACTTATCGAATACA 21

RESULT 9
US-10-068-067-22
; Sequence 22, Application US/10068067
; Publication No. US20020151064A1
; GENERAL INFORMATION:
; APPLICANT: Rothenberg, Marc E.
; APPLICANT: Zimmermann, Nives
; TITLE OF INVENTION: REGULATION OF CCR3 EXPRESSION
; FILE REFERENCE: CMC-153
; CURRENT APPLICATION NUMBER: US/10/068,067
; CURRENT FILING DATE: 2002-02-05
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-068-067-22

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Best Local Similarity 61.9%; Pred. No. 0.018;
Matches 13; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACCACTGGTCTTCTGTGC 21
DB 1 GGUACCACUGGUCUUGUG 21

RESULT 10
US-10-068-067-24
; Sequence 24, Application US/10068067
; Publication No. US20020151064A1
; GENERAL INFORMATION:
; APPLICANT: Rothenberg, Marc E.
; APPLICANT: Zimmermann, Nives
; TITLE OF INVENTION: REGULATION OF CCR3 EXPRESSION
; FILE REFERENCE: CMC-153
; CURRENT APPLICATION NUMBER: US/10/068,067
; CURRENT FILING DATE: 2002-02-05
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 24
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; LENGTH: 265
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; OTHER INFORMATION: Clone ID: 37-LIB188-012-Q1-E1-B2
US-09-983-965-304

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Db 217 CTTGTGCTTATCCGGG 202

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; Sequence 67946, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 67946
; LENGTH: 465
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_68757C.1
US-10-437-963-67946

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Db 120 CAAGAACTTATCGAAA 135

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 18:10:40 ; Search time 51.4397 Seconds

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Perfect score: 51

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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:**
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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	16	31.4	21	4	US-09-422-978-9067
3	16	31.4	698	4	US-09-634-238-126
4	15	29.4	2254	2	US-08-635-066-1
5	15	29.4	2787	4	US-09-134-000C-3185
6	15	29.4	3177	3	US-09-134-513-1
7	15	29.4	8920	2	US-08-446-855A-1
8	15	29.4	8920	3	US-09-150-741-1
9	15	29.4	11867	4	US-09-497-855A-32
10	14	27.5	281	4	US-08-469-260A-18
11	14	27.5	281	4	US-08-469-260A-20
12	14	27.5	281	4	US-08-488-446-18
13	14	27.5	281	4	US-08-488-446-20
14	14	27.5	281	4	US-08-467-344A-18
15	14	27.5	281	4	US-08-467-344A-20
16	14	27.5	435	4	US-09-489-039A-6593
17	14	27.5	462	4	US-09-621-976-15146
18	14	27.5	479	4	US-08-469-260A-25
19	14	27.5	479	4	US-08-469-260A-392
20	14	27.5	479	4	US-08-488-446-25
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23	14	27.5	479	4	US-08-467-344A-392
24	14	27.5	495	4	US-09-621-976-17953
25	14	27.5	508	4	US-09-621-976-9046
26	14	27.5	513	4	US-09-621-976-3690
27	14	27.5	517	4	US-09-621-976-1231

c	28	14	27.5	542	4	US-09-669-751-135	Sequence 135, App
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c	34	14	27.5	1267	4	US-09-280-428A-9	Sequence 9, Appli
c	35	14	27.5	1301	4	US-09-489-847-108	Sequence 108, App
c	36	14	27.5	1456	4	US-09-064-411A-23	Sequence 23, Appl
c	37	14	27.5	1578	4	US-09-252-991A-5039	Sequence 5039, Ap
c	38	14	27.5	1581	4	US-09-252-991A-5177	Sequence 5177, Ap
c	39	14	27.5	1760	4	US-09-495-050A-139	Sequence 139, App
c	40	14	27.5	2114	4	US-09-370-838-158	Sequence 158, App
c	41	14	27.5	2432	4	US-09-205-258-48	Sequence 48, Appl
c	42	14	27.5	2793	4	US-08-753-750B-1	Sequence 1, Appli
c	43	14	27.5	3142	1	US-08-110-158-3	Sequence 3, Appli
c	44	14	27.5	3142	4	US-09-023-655-1090	Sequence 1090, Ap
c	45	14	27.5	3144	5	PCT-US91-05059-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-08-720-565-3
; Sequence 3, Application US/08720565
; Patent No. 6537764
; GENERAL INFORMATION:
; APPLICANT: Gerard, Craig J.
; APPLICANT: Gerard, NO. 6537764ma P.
; APPLICANT: Mackay, Charles R.
; APPLICANT: Pomath, Paul D.
; APPLICANT: Post, Theodore W.
; APPLICANT: Qin, Shixin
; TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTOR GENE CCR3 AND
; TITLE OF INVENTION: ANTAGONISTS THEREOF
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/720,565
; FILING DATE: 30-SEP-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/00608
; FILING DATE: 19-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/375,199
; FILING DATE: 19-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: LKS94-05A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1193 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: Double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

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;
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: 92..1156
; US-08-720-565-3

Query Match      68.6%; Score 35; DB 4; Length 1193;
Best Local Similarity 100.0%; Pred. No. 4.1e-10;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 TTGTGCTTATCCGGGCAAGAACTTATCGAAATACA 51
Db 1 TTGTGCTTATCCGGGCAAGAACTTATCGAAATACA 35

RESULT 2
US-09-422-978-9067
; Sequence 9067, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 9067
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..21_bind
; OTHER INFORMATION: downstream amplification primer 99-2170 for SEQ 1202, in complete
; US-09-422-978-9067

Query Match      31.4%; Score 16; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GGTCTTCTTGCTTGA 25
Db 1 GGTCTTCTTGCTTGA 16

RESULT 3
US-09-634-238-126
; Sequence 126, Application US/09634238
; Patent No. 6544772
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Havukkala, Ilkka J.
; APPLICANT: Bloksberg, Leonard, N.
; APPLICANT: Lubbers, Mark W.
; APPLICANT: Dekker, James
; APPLICANT: Christenson, Anna C.
; APPLICANT: Holland, Ross
; APPLICANT: O'Toole, Paul W.
; APPLICANT: Reid, Julian R.
; APPLICANT: Coolbear, Timothy
; TITLE OF INVENTION: Polynucleotides, materials incorporating
; FILE REFERENCE: them and methods for using them.
; CURRENT FILING DATE: 2000-08-08
; NUMBER OF SEQ ID NOS: 422

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126
; LENGTH: 698
; TYPE: DNA
; ORGANISM: Lactobacillus rhamnosus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(698)
; OTHER INFORMATION: n = A,T,C or G
; US-09-634-238-126

Query Match      31.4%; Score 16; DB 4; Length 698;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TGGTCTTCTTGCTT 24
Db 550 TGGTCTTCTTGCTT 565

RESULT 4
US-08-635-066-1
; Sequence 1, Application US/08635066
; Patent No. 5945580
; GENERAL INFORMATION:
; APPLICANT: Dunsmuir, Pamela
; APPLICANT: Harpster, Mark H.
; TITLE OF INVENTION: Capsicum Hemicellulase Polynucleotides
; TITLE OF INVENTION: and Polypeptides
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/635,066
; FILING DATE: 19-APR-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 012176-005500
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2254 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 609..2129
; US-08-635-066-1

Query Match      29.4%; Score 15; DB 2; Length 2254;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 TCTTCTTGTGCTTAT 26
Db 643 TCTTCTTGTGCTTAT 657
```

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RESULT 5
US-09-134-000C-3185/c
; Sequence 3185, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032798-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3185
; LENGTH: 2787
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-3185

Query Match      29.4%; Score 15; DB 4; Length 2787;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 GGTCTTCTTGTCCT 24
        |||||
DB      2353 GGTCTTCTTGTCCT 2339

RESULT 6
US-09-134-513-1
; Sequence 1, Application US/09134513
; Patent No. 6210964
; GENERAL INFORMATION:
; APPLICANT: Brown, Edward M.
; APPLICANT: Diaz, Ruben
; APPLICANT: Bai, Mei
; APPLICANT: Quinn, Stephen J.
; TITLE OF INVENTION: The Avian Extracellular Calcium-Sensing
; TITLE OF INVENTION: Receptor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Vinson & Elkins L.L.P.
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.
; ZIP: 20004-1008
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,513
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanzo, Michael A.
; REGISTRATION NUMBER: 36,912
; REFERENCE/DOCKET NUMBER: BRI331/13003
; TELEPHONE: (202)639-6585
; TELEFAX: (202)639-6604
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
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; HYPOTHETICAL: NO
US-09-134-513-1

Query Match      29.4%; Score 15; DB 3; Length 3177;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CTGGTCTTCTTGTC 22
        |||||
DB      2176 CTGGTCTTCTTGTC 2190

RESULT 7
US-08-446-855A-1
; Sequence 1, Application US/08446855A
; Patent No. 5849573
; GENERAL INFORMATION:
; APPLICANT: Stewart, Thomas S
; APPLICANT: Flores, Maria V
; APPLICANT: O'Sullivan, William J
; TITLE OF INVENTION: Nucleotide sequence encoding carbamoyl
; TITLE OF INVENTION: phosphate synthetase II
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderhye PC
; STREET: 1100 No. 5849573th Glebe Road, 8th Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,855A
; FILING DATE: 06-Jul-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mitchard, Leonard C
; REGISTRATION NUMBER: 29,009
; REFERENCE/DOCKET NUMBER: 47-80
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8920 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic
US-08-446-855A-1

Query Match      29.4%; Score 15; DB 2; Length 8920;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      33 AAGAACTTATCGAAA 47
        |||||
DB      3831 AAGAACTTATCGAAA 3845

RESULT 8
US-09-150-741-1
; Sequence 1, Application US/09150741
; Patent No. 6183996
; GENERAL INFORMATION:
; APPLICANT: Stewart et al.
; TITLE OF INVENTION: Nucleotide Sequence Encoding Carbamoyl Phosphate
; Patent No. 6183996
; TITLE OF INVENTION: Synthetase II
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; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/150,741
; CURRENT FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: PL6380
; EARLIER FILING DATE: 1992-12-16
; EARLIER APPLICATION NUMBER: AU93/00617
; EARLIER FILING DATE: 1993-12-02
; EARLIER APPLICATION NUMBER: 08/446,855
; EARLIER FILING DATE: 1995-07-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 8920
; TYPE: DNA
; ORGANISM: Plasmodium falciparum
US-09-150-741-1

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```

Query Match          29.4%; Score 15; DB 3; Length 8920;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 33 AAGAACTTATCGAAA 47
Db 3831 AAGAACTTATCGAAA 3845

```

```

RESULT 9
US-09-497-855A-32/c
; Sequence 32, Application US/09497855A
; Patent No. 6605432
; GENERAL INFORMATION:
; APPLICANT: Huang, Tim
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
; FILE REFERENCE: UMO1523
; CURRENT APPLICATION NUMBER: US/09/497,855A
; CURRENT FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/120,592
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 60/118,760
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 118067
; TYPE: DNA
; ORGANISM: Homo sapiens;
US-09-497-855A-32

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Query Match          29.4%; Score 15; DB 4; Length 118067;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 3 TACCACTGGTCTTCT 17
Db 113196 TACCACTGGTCTTCT 113182

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RESULT 10
US-08-469-260A-18
; Sequence 18, Application US/08469260A
; Patent No. 6451578
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS

```

```

; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,260A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-469-260A-18

```

```

Query Match          27.5%; Score 14; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 1e-02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 26 TCCGGGCAAGAACT 39
Db 213 TCCGGGCAAGAACT 226

```

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RESULT 11
US-08-469-260A-20
; Sequence 20, Application US/08469260A
; Patent No. 6451578
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICANT: US/08/469,260A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: POREBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-469-260A-20

Query Match 27.5%; Score 14; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 TCCGGGCAAGAACT 39
|||||
DB 213 TCCGGGCAAGAACT 226

RESULT 12

US-08-488-446-18
Sequence 18, Application US/08488446
Patent No. 6558898
GENERAL INFORMATION:
APPLICANT: JOHN N. SIMONS
APPLICANT: TAMI J. PILOT-MATIAS
APPLICANT: GEORGE J. DAWSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUEHROFF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BULJK
APPLICANT: ISA K. MUSHAWAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,446
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550
FILING DATE:
ATTORNEY/AGENT INFORMATION:

NAME: POREBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-488-446-18
Query Match 27.5%; Score 14; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 26 TCCGGGCAAGAACT 39
|||||
DB 213 TCCGGGCAAGAACT 226
RESULT 13
US-08-488-446-20
Sequence 20, Application US/08488446
Patent No. 6558898
GENERAL INFORMATION:
APPLICANT: JOHN N. SIMONS
APPLICANT: TAMI J. PILOT-MATIAS
APPLICANT: GEORGE J. DAWSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUEHROFF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BULJK
APPLICANT: ISA K. MUSHAWAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,446
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: POREBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

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; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-467-344A-18
; Sequence 18, Application US/08467344A
; Patent No. 6586568
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; TAMI J. PILOT-MATIAS
; GEORGE J. DAWSON
; GEORGE G. SCHLAUDER
; SURESH M. DESAI
; THOMAS P. LEARY
; ANTHONY SCOTT MUERHOFF
; JAMES C. ERKER
; SHERI L. BUIJK
; ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 07-Jun-1995
; APPLICATION NUMBER: US/08/467,344A
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/424,550
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-08-467-344A-18
Query Match 27.5%; Score 14; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 TCCGGGCAAGAACT 39
|||||
Db 213 TCCGGGCAAGAACT 226

RESULT 14
US-08-467-344A-18
; Sequence 18, Application US/08467344A
; Patent No. 6586568
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; TAMI J. PILOT-MATIAS
; GEORGE J. DAWSON
; GEORGE G. SCHLAUDER
; SURESH M. DESAI
; THOMAS P. LEARY
; ANTHONY SCOTT MUERHOFF
; JAMES C. ERKER
; SHERI L. BUIJK
; ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 07-Jun-1995
; APPLICATION NUMBER: US/08/467,344A
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/424,550
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-08-467-344A-18
Query Match 27.5%; Score 14; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 TCCGGGCAAGAACT 39
|||||
Db 213 TCCGGGCAAGAACT 226

RESULT 15
US-08-467-344A-20
; Sequence 20, Application US/08467344A
; Patent No. 6586568
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; TAMI J. PILOT-MATIAS
; GEORGE J. DAWSON
; GEORGE G. SCHLAUDER
; SURESH M. DESAI
; THOMAS P. LEARY
; ANTHONY SCOTT MUERHOFF
; JAMES C. ERKER
; SHERI L. BUIJK
; ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 07-Jun-1995
; APPLICATION NUMBER: US/08/467,344A
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/424,550
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-08-467-344A-20
Query Match 27.5%; Score 14; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 TCCGGGCAAGAACT 39
|||||
Db 213 TCCGGGCAAGAACT 226

Search completed: August 2, 2004, 20:30:02
Job time : 52.4397 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 18:06:45 ; Search time 2107.71 Seconds

(without alignments)
722.573 Million cell updates/sec

Title: US-10-068-067-16

Perfect score: 51

Sequence: 1 ggtaccactgtcttttgtt.....caagaacttatcgaaataca 51

Scoring table: OLIGO.NUC

Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_estbam:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_nam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gsl:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	70.6	876	12	BI906283
2	18	35.3	584	14	CB390728
3	17	33.3	196	10	BF153648
4	17	33.3	406	28	B40772

5	17	33.3	510	14	CD923067
6	17	33.3	523	12	BM375216
7	17	33.3	537	10	AW221092
8	17	33.3	577	9	AI772554
9	17	33.3	577	12	BG133271
10	17	33.3	598	29	CNS07HW5
11	17	33.3	610	14	CD925736
12	17	33.3	613	28	BH299085
13	17	33.3	647	12	BM160641
14	17	33.3	648	10	AW945046
15	17	33.3	672	14	CD911444
16	17	33.3	690	29	CE306183
17	17	33.3	780	29	CC506531
18	17	33.3	787	14	CD911445
19	17	33.3	905	10	BF340232
20	17	33.3	1203	12	BI764950
21	17	33.3	1828	12	BG297964
22	16	31.4	169	9	AV162852
23	16	31.4	212	13	BQ282503
24	16	31.4	221	10	BF557219
25	16	31.4	224	9	AA957733
26	16	31.4	288	9	AV340346
27	16	31.4	318	29	CG407599
28	16	31.4	322	10	AW826871
29	16	31.4	346	12	BG738607
30	16	31.4	364	10	BF389025
31	16	31.4	404	10	BE344124
32	16	31.4	404	28	AQ825343
33	16	31.4	406	9	AI112888
34	16	31.4	406	14	CD489747
35	16	31.4	420	29	CE669510
36	16	31.4	422	13	BX307267
37	16	31.4	430	14	CD489612
38	16	31.4	433	14	CB495381
39	16	31.4	433	14	CB495414
40	16	31.4	433	14	CB495567
41	16	31.4	436	13	BQ282505
42	16	31.4	451	13	BY505647
43	16	31.4	456	10	BF388753
44	16	31.4	456	10	BF388753
45	16	31.4	458	14	CD489171

ALIGNMENTS

BI906283 603063222F1 NIH_MGC_118 Homo sapiens cdna clone IMAGE:5212541 5',
mRNA sequence. linear EST 16-OCT-2001
BI906283
ACCESSION BI906283.1 GI:16168946
VERSION BI906283
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 876)
NIH-VGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: ILAM11533 row: k column: 06
High quality sequence stop: 800.

FEATURES
source

Location/Qualifiers
1. 876
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5212541"
/tissue_type="leukocyte"
/lab_host="DH10B"
/clone_lib="NIH_MGC_118"
/note="vector: pCMV-SPORT6; Site:1: NotI; Site:2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 70.6%; Score 36; DB 12; Length 876;
Best Local Similarity 100.0%; Pred. No. 1.5e+08;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 CTGTGCTTATCCGGCGAAGACTTATCGAATACA 51
|||||
Db 1 CTGTGCTTATCCGGCGAAGACTTATCGAATACA 36

RESULT 2
LOCUS

CB390728 584 bp mRNA linear EST 15-MAY-2003
DEFINITION OSTF139F9.1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.

ACCESSION CB390728

VERSION CB390728.1 GI:30732438

KEYWORDS EST.

SOURCE Caenorhabditis elegans

ORGANISM Caenorhabditis elegans

REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;

Rhabditoides; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 584)

Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M.,

Armstrong, C.M., Li, S., Jacotot, L., Bustin, N., Janky, R., Moore, T.,

Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,

Endress, G.A., Jemma, S., Chevet, E., Papasotiropoulos, V.,

Tolias, P.P., Pracek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,

Doucette-Stamm, L., Hill, D.E. and Vidal, M.

C. elegans ORFome version 1.1: experimental verification of the

genome annotation and resource for proteome-scale protein

expression

Nat. Genet. (2003) In press

Contact: Vidal M

Marc Vidal Laboratory

Dana Farber Cancer Institute

1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 5739

Email: Marc.Vidal@dfci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were

designed on the predicted protein encoding ORF. C. elegans ORFome

cloning project : Contact David Hill@dfci.harvard.edu or

marc.vidal@dfci.harvard.edu

POLYA-No. Location/Qualifiers

1. 584

/organism="Caenorhabditis elegans"

/mol_type="mRNA"

/strain="N2"

/db_xref="taxon:6239"

/sex="Hermaphrodite and male"

/tissue_type="whole animal"

/dev_stage="mixed stage"

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FEATURES
source

Location/Qualifiers
1. 876
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="IMAGE:5212541"
/tissue_type="leukocyte"
/lab_host="DH10B"
/clone_lib="NIH_MGC_118"
/note="vector: pCMV-SPORT6; Site:1: NotI; Site:2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 70.6%; Score 36; DB 12; Length 876;
Best Local Similarity 100.0%; Pred. No. 1.5e+08;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 CTGTGCTTATCCGGCGAAGACTTATCGAATACA 51
|||||
Db 1 CTGTGCTTATCCGGCGAAGACTTATCGAATACA 36

FEATURES
source

Location/Qualifiers
1. 876
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5212541"
/tissue_type="leukocyte"
/lab_host="DH10B"
/clone_lib="NIH_MGC_118"
/note="vector: pCMV-SPORT6; Site:1: NotI; Site:2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 35.3%; Score 18; DB 14; Length 584;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 TGTGCTTATCCGGCAAG 35
|||||
Db 233 TGTGCTTATCCGGCAAG 250

RESULT 3
LOCUS

BF153648 196 bp mRNA linear EST 11-SEP-2002
DEFINITION 032A04 Mature tuber lambda ZAP Solanum tuberosum cDNA 5', mRNA

ACCESSION BF153648

VERSION BF153648.1 GI:11035588

KEYWORDS EST.

SOURCE Solanum tuberosum (potato)

ORGANISM Solanum tuberosum

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; lamids; Solanales; Solanaceae; Solanum.

1 (bases 1 to 196)

Crookshanks, M., Emmersen, J., Welinder, K.G. and Nielsen, K.L.

The potato tuber transcriptome: analysis of 6077 expressed sequence

tags

JOURNAL FEBS Lett. 506 (2), 123-126 (2001)

MEDLINE 21475600

PUBMED 11591384

COMMENT Contact: Karen G. Welinder

Institut for bioteknologi

Aalborg Universitet

Sohngaardsholmsvej 49, 9000 Aalborg, Denmark

Tel: +45 96358467

Fax: +45 98141808

Email: kgw@bio.auc.dk

High quality sequence stop: 196

POLYA-No. Location/Qualifiers

1. 196

/organism="Solanum tuberosum"

/mol_type="mRNA"

/cultivar="Field grown Kurat"

/db_xref="taxon:4113"

/tissue_type="tuber"

/clone_lib="Mature tuber lambda ZAP"

/note="Vector: Lambda ZAP"

ORIGIN

Query Match 33.3%; Score 17; DB 10; Length 196;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 TTCTTGCTTATCCGG 30
|||||
Db 153 TTCTTGCTTATCCGG 137

RESULT 4

B40772

LOCUS

DEFINITION

HS-1052-B1-A05-MF.abi CIT Human Genomic Sperm Library C Homo

sapiens genomic clone Plate=CT 774 Col=9 Row=B, genomic survey

sequence.

ACCESSION B40772

VERSION B40772.1 GI:2545024

Query Match 33.3%; Score 17; DB 10; Length 196;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 TTCTTGCTTATCCGG 30
|||||
Db 153 TTCTTGCTTATCCGG 137

Query Match 33.3%; Score 17; DB 10; Length 196;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 TTCTTGCTTATCCGG 30
|||||
Db 153 TTCTTGCTTATCCGG 137

Query Match 33.3%; Score 17; DB 10; Length 196;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 TTCTTGCTTATCCGG 30
|||||
Db 153 TTCTTGCTTATCCGG 137


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KEYWORDS
SOURCE  Homo sapiens (human)
ORGANISM

REFERENCE
AUTHORS  Mahairas,G.G., Zackrone,K.D., Smith,T., Tipton,S., Schmidt,S.,
          Traicoff,R., Abajian,C., Blanchard,A., West,A. and Hood,L.E.
TITLE    Construction of a Characterized Clone Resource for Genomic
          Sequencing: Generation and Preliminary Analysis of 20,000 Sequence
          Tagged Connectors
JOURNAL  Unpublished (1997)
COMMENT  Contact: Mahairas GG, Zackrone KD, Hood L
          University of Washington
          Seattle, WA 98195, USA
          Tel: (206) 616-8744
          Fax: (206) 685-7301
          Email: kzackrone@u.washington.edu
          Sequence Tagged Connector
          Plate: CT 774 row: B column: 9
          Class: BAC ends
          High quality sequence stop: 406.
          Location/Qualifiers
FEATURES
source
1..406
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=CT 774 Col=9 Row=B"
/sex="M"
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/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
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ORIGIN
Query Match 33.3%; Score 17; DB 28; Length 406;
Best Local Similarity 100.0%; Pred.No.1.7e+02; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0;

Qy 11 GTCCTCTTGCTGCTTATC 27
Db 85 GTCCTCTTGCTGCTTATC 101

RESULT 5
CD923067 510 bp mRNA linear EST 15-JUL-2003
LOCUS G750.106G07F010531 G750 Triticum aestivum cDNA clone G750106G07,
DEFINITION mRNA sequence.
ACCESSION CD923067
VERSION CD923067.1 GI:32770831
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 510)
AUTHORS Genoplante.
TITLE Genoplante, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplante
          93, rue Henri Rochefort 91025 EVRY CEDEX France
          Tel: 33 1 69 47 54 00
          Fax: 33 1 69 47 54 10
          This sequence has been generated in the framework of the french
          plant genomics programme 'Genoplante' (http://www.genoplante.com
          and http://genoplante-info.infobiogen.fr).
          Location/Qualifiers
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/cultivar="recital"

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Best Local Similarity 100.0%; Pred.No.1.7e+02; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0;

Qy 12 TCTCTTGCTGCTTATCC 28
Db 73 TCTCTTGCTGCTTATCC 89

RESULT 6
BM375216 523 bp mRNA linear EST 23-JUL-2002
LOCUS EBem06 SQ002 L05_R embryo, 21 DPA, no treatment, cv Optic, EBem06
DEFINITION Hordeum vulgare subsp. vulgare cDNA clone EBem06_SQ002_L05 5', mRNA
          sequence.
ACCESSION BM375216
VERSION BM375216.2 GI:21935188
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 523)
AUTHORS Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudie,S., Cardle,L.,
          Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,R.
TITLE Development of Barley Transcriptome Resources
JOURNAL Unpublished (2001)
COMMENT On Jan 10, 2002 this sequence version replaced gi:18118606.
          Contact: Waugh R, Marshall D
          Genome Dynamics/Computational Biology
          Scottish Crop Research Institute
          Invergowrie, Dundee, DD2 5DA, Scotland, UK
          Tel: 00 44 1382 562731
          Fax: 00 44 1382 562426
          Email: est@scri.sari.ac.uk
          All sequence has a Phred quality score of 20 or over
          Seq primer: M13 reverse.
          Location/Qualifiers
FEATURES
source
1..523
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
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/db_xref="taxon:112509"
/clone="EBem06_SQ002_L05"
/tissue_type="embryo"
/dev_stage="21 DPA"
/lab_host="DH10B"
/clone_lib="embryo, 21 DPA, no treatment, cv Optic,
EBem06"
/note="Vector: pSPORT1; Site:1: Sal I; Site 2: Not I;
Non-normalised library, directionally cloned into pSPORT1.
Derived from embryos dissected from developing grains (21
days post anthesis) in glasshouse grown barley plants.
Developed as part of the barley transcriptome resources of
BBSRC/SEERAD funded cereal IGF (Investigating Gene
Function) project."
ORIGIN
Query Match 33.3%; Score 17; DB 12; Length 523;
Best Local Similarity 100.0%; Pred.No.1.7e+02; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0;

Qy 12 TCTCTTGCTGCTTATCC 28

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Db 188 TCTCTGTGCTTATCCG 172

RESULT 7 AW221092/c

LOCUS AW221092 537 bp mRNA linear EST 18-MAY-2001
DEFINITION EST297561 tomato fruit mature green, TAMU Lycopersicon esculentum
CDNA clone cLEF12D1, mRNA sequence.

ACCESSION AW221092
VERSION AW221092.1 GI:6532776
KEYWORDS EST.

SOURCE Lycopersicon esculentum (tomato)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.

REFERENCE 1 (bases 1 to 537)

Aucala, J., Vrebalov, J., White, R., Matern, A.L., Holt, I.E., Liang, F.,
Upton, J., Hansen, T., Craven, M.B., Bowman, C.L., Ahn, S.,
Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and
Giovannoni, J.

Generation of ESTs from tomato fruit tissue

Unpublished (1999)

Contact: CUGI

Clemson University

Clemson University Genomics Institute

100 Jordan Hall, Clemson, SC 29634, USA

Email: <http://www.genome.clemson.edu/orders/index.html>

5 prime sequence.

Location/Qualifiers

1..537
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEF12D1"
/tissue_type="fruit pericarp"
/dev_stage="mature green (3-5 days pre-ripening)"
/lab_host="SOLR"
/clone_lib="tomato fruit mature green, TAMU"
/notes="Vector: pBlueScript SK(-); Site_1: EcoRI; Site_2:
XhoI; cLEF - Fruit were tagged at the 1cm stage and
harvested 3-5 days prior to ripening. Fruit were cut in
half to verify the seeds were indeed 'immature' and the
seeds and locules were discarded prior to freezing the
pericarp"

ORIGIN

Query Match 33.3%; Score 17; DB 10; Length 537;
Best Local Similarity 100.0%; Pred. NO. 1.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TCTCTGTGCTTATCCG 30

Db 260 TCTCTGTGCTTATCCG 244

RESULT 8 AI772554/c

LOCUS AI772554 577 bp mRNA linear EST 18-MAY-2001
DEFINITION EST253654 tomato resistant, Cornell Lycopersicon esculentum CDNA
clone cLER3E11, mRNA sequence.

ACCESSION AI772554

VERSION AI772554.1 GI:5270595

KEYWORDS EST.

SOURCE Lycopersicon esculentum (tomato)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.

REFERENCE 1 (bases 1 to 577)

D'Ascenzo, M., He, X., Lyman, J., Matern, A.L., Vision, T., Holt, I.E.,
Liang, F., Upton, J., Ronning, C.M., Craven, M.B., Fujii, C.Y.,

Bowman, C.L., Nierman, W., Fraser, C.M., Venter, J.C., Tanksley, S.D.,
Giovannoni, J.J. and Martin, G.B.

Generation of ESTs from *Pseudomonas* resistant tomato

Unpublished (1999)

Contact: CUGI

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Email: <http://www.genome.clemson.edu/orders/index.html>

5 prime sequence.

Location/Qualifiers

1..577
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="Ril-12 (35S::Pto in Rio Grande x Money Maker)"
/db_xref="taxon:4081"
/clone="cLER3E11"
/tissue_type="leaf"
/dev_stage="4-week old"
/lab_host="SOLR"
/clone_lib="tomato resistant, Cornell"
/notes="Vector: pBlueScript SK(-); Site_1: EcoRI; Site_2:
XhoI; cLER - Tomato *Pseudomonas* resistant EST library.
Directionally cloned cDNAs inserted into pBlueScript
SK(-) at 5' end with EcoRI and 3' end with XhoI site."

ORIGIN

Query Match 33.3%; Score 17; DB 9; Length 577;
Best Local Similarity 100.0%; Pred. NO. 1.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TCTCTGTGCTTATCCG 30

Db 56 TCTCTGTGCTTATCCG 50

RESULT 9 BG133271/c

LOCUS BG133271 577 bp mRNA linear EST 31-JAN-2001
DEFINITION EST466163 tomato crown gall Lycopersicon esculentum CDNA clone
CTOE1116 5' sequence, mRNA sequence.

ACCESSION BG133271

VERSION BG133271.1 GI:12633459

KEYWORDS EST.

SOURCE Lycopersicon esculentum (tomato)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.

REFERENCE 1 (bases 1 to 577)

van der Hoeven, R., Sun, H., Cho, J., Utterback, T., Hansen, C.,

Ronning, C. and Tanksley, S.

Generation of ESTs from tomato crown gall tissue

Unpublished (2001)

Contact: CUGI

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Email: <http://www.genome.clemson.edu/orders/index.html>.

Location/Qualifiers

1..577
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="CTOE1116"
/tissue_type="crown gall"
/dev_stage="crown galls from full-grown plants (8 wks
old)"
/lab_host="SOLR"
/clone_lib="tomato crown gall"
/notes="Vector: pBlueScript SK(-); Site_1: EcoRI; Site_2:
XhoI; Four wk old greenhouse plants were stab inoculated

on stem with Agrobacterium tumefaciens C58 (Dr. T.J. Burr, Cornell U.). Galls were allowed to develop for another 4 wks, when gall tissue was frozen in liquid nitrogen."

ORIGIN

Query Match 33.3%; Score 17; DB 12; Length 577;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 TTCTTGCTGCTTATCCGG 30
Db 150 TTCTTGCTGCTTATCCGG 134

RESULT 10

CNS07HW5/c

LOCUS 598 bp DNA linear GSS 03-OCT-2001
DEFINITION Anopheles gambiae GSS T7 end of clone 31B05 of library NotreDamel from strain PEST of Anopheles gambiae (African malaria mosquito), genomic survey sequence.

ACCESSION AL611591

VERSION AL611591.1 GI:15963014

KEYWORDS GSS.

SOURCE Anopheles gambiae (African malaria mosquito)

ORGANISM Anopheles gambiae

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;

Anopheles.

REFERENCE 1 (bases 1 to 598)

AUTHORS Direct Submission

JOURNAL Submitted (01-OCT-2001) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

REFERENCE 2 (bases 1 to 598)

AUTHORS Roth,C.W., Brey,P.T., Ke,Z. and Collins,F.H.

TITLE Direct Submission

JOURNAL Submitted (01-OCT-2001) BEMT, Institut Pasteur, 25, rue du Dr.

Roux, Paris 75015, France

This clone is from an A. Gambiae BAC library provided by F.H.

Collins and sequenced by Genoscope in collaboration with the

Laboratory of Biochem. and Biol. Molec. of Insects, Institut

Pasteur.

FEATURES

source

1..598

/organism="Anopheles gambiae"

/mol_type="genomic DNA"

/strain="PEST"

/db_xref="taxon:7165"

/clone="31B05"

/clone_lib="NotreDamel"

/note="end : 17"

ORIGIN

Query Match 33.3%; Score 17; DB 29; Length 598;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 CTCTTGCTGCTTATCCG 29
Db 75 CTCTTGCTGCTTATCCG 59

RESULT 11

CD925736

LOCUS 610 bp mRNA linear EST 15-JUL-2003

DEFINITION G750.118H11F010711 G750 Triticum aestivum cDNA clone G750118H11, mRNA sequence.

ACCESSION CD925736

VERSION CD925736.1 GI:32773500

KEYWORDS EST.

SOURCE Triticum aestivum (bread wheat)

ORGANISM Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.

1 (bases 1 to 610)

Genoplatte.

Genoplatte, a major partnership french program in plant genomics

Unpublished (2003)

Contact: Genoplatte

Genoplatte

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french

plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>

and <http://genoplatte-info.infobiogen.fr>).

FEATURES

source

1..610

/organism="Triticum aestivum"

/mol_type="mRNA"

/cultivar="recital"

/db_xref="taxon:4565"

/clone="G750118H11"

/tissue_type="grain (750 degrees per day after

pollination)"

/clone_lib="G750"

ORIGIN

Query Match 33.3%; Score 17; DB 14; Length 610;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 TCTTCTTGCTTATCC 28

Db 320 TCTTCTTGCTTATCC 336

RESULT 12

BH299085/c

LOCUS 613 bp DNA linear GSS 30-NOV-2001

DEFINITION CH230-146H22.TU CHORI-230 Segment 1 Rattus norvegicus genomic clone

CH230-146H22, genomic survey sequence.

ACCESSION BH299085

VERSION BH299085.1 GI:17211493

KEYWORDS GSS.

SOURCE Rattus norvegicus (Norway rat)

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 613)

Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K.,

Shvartsbeyn,A., Gebregeorgis,B., Overton,L., Russell,D., Chen,D.,

Riggs,F., de Jong,P. and Fraser,C.W.

Rat BAC End Sequences from Library CHORI-230 EcoRI segment

Unpublished (1999)

Other GSSs: CH230-146H22.TV

Contact: Shaving Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230

(<http://www.chori.org/bacpac/rat230.htm>). For BAC library

availability, please contact Pieter de Jong (pdj@jgnc.org).

Clones may be purchased from BACPAC Resources

(<http://www.chori.org/bacpac/orering.information.htm>). BAC end

plate: 146 row: H column: 22

Seq primer: SP6

Class: BAC ends.

FEATURES

Location/Qualifiers

```

source
1. .613
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-146H22"
/sex="Female"
/cell_type="Brain"
/clone_lib="CHORI-230 Segment 1"
/note="vector: pTARAC2.1; Site 1: EcoRI; Site 2: EcoRI;
CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
Pieter de Jong"

ORIGIN
Query Match 33.3%; Score 17; DB 28; Length 613;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCACTGCTCTCTGTG 21
| | | | | | | | | | | | | | | | | | | | |
Db 172 CCACTGCTCTCTGTG 156

RESULT 13
BM160641 647 bp mRNA linear EST 04-DEC-2001
DEFINITION EST563164 PYBS Plasmodium yoelii yoelii cDNA clone PYCUT89 5' end,
mRNA sequence.
ACCESSION BM160641
VERSION BM160641.1 GI:17306322
KEYWORDS EST.
SOURCE Plasmodium yoelii yoelii
ORGANISM Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE 1 (bases 1 to 647)
AUTHORS Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,A.B.,
Fraser,C.M. and Carucci,D.J.
TITLE Plasmodium yoelii EST project at TIGR
JOURNAL Unpublished (2001)
COMMENT Contact: Jane Carlton
Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-530-9319
Fax: 301-838-0208
Email: carlton@tigr.org
For clone info, please contact the Malaria Research and Reference
Reagent Resource Center, ATCC
http://www.malaria.mr4.org/mr4pages/index.html
Seq primer: ADF.

FEATURES
Location/Qualifiers
source
1. .647
/organism="Plasmodium yoelii yoelii"
/mol_type="mRNA"
/strain="17XL"
/sub_species="yoelii"
/db_xref="taxon:73239"
/clone="PYCUT89"
/dev_stage="Asexual blood stages"
/lab_host="E. coli XL-1 Blue"
/clone_lib="PyBS"
/note="vector: PAD-GAL4; At 20-25% parasitemia, blood was
collected from BALB/cBYJ mice infected with Py17XL
parasites, and leukocytes removed by passage over
microcrystalline cellulose columns. Total RNA was
isolated using the guanidinium isothiocyanate method, and
mRNA isolated using oligo(dT)-cellulose chromatography.
First strand cDNA synthesis was completed using a 50-base
primer and reverse transcriptase in the presence of
5-methyl dCTP. After second strand synthesis, uneven
termini were treated with Pfu DNA polymerase and EcoRI
adaptors ligated to the blunt ends. The sample was cleaved
with XhoI and separated on a Sephacryl S-500 column.

```

```

ORIGIN
Query Match 33.3%; Score 17; DB 12; Length 647;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 35 GAACCTTATCGAATACA 51
| | | | | | | | | | | | | | | | | | | | |
Db 139 GAACCTTATCGAATACA 155

RESULT 14
AW945046 648 bp mRNA linear EST 18-MAY-2001
DEFINITION EST337096 tomato flower buds 3-8 mm, Cornell University
Lycopersicon esculentum cDNA clone cTOB12P18 5', mRNA sequence.
ACCESSION AW945046
VERSION AW945046.1 GI:8122797
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
REFERENCE 1 (bases 1 to 648)
AUTHORS van der Hoeven,R.S., Bezzzredes,J.L., Matern,A.L., Holt,I.E.,
Liang,F., Hansen,I., Craven,M.B., Bowman,C.L., Romning,C.M.,
Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and
Tanksley,S.D.
TITLE Generation of ESTs from tomato flower tissue, 3-8 mm buds
JOURNAL Unpublished (1999)
COMMENT Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.

FEATURES
Location/Qualifiers
source
1. 648
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cTOB12P18"
/tissue_type="flower"
/dev_stage="3-8mm buds"
/clone_lib="tomato flower buds 3-8 mm, Cornell University"
/note="vector: Bluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; supplier: Tanksley; Flower buds and flowers were
taken from greenhouse plants (4-8 wks old, TA496). They
were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."

ORIGIN
Query Match 33.3%; Score 17; DB 10; Length 648;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 TTCTTGCTTATCCGG 30
| | | | | | | | | | | | | | | | | | | | |
Db 141 TTCTTGCTTATCCGG 125

RESULT 15
CD911444 672 bp mRNA linear EST 14-JUL-2003
DEFINITION G550.111C10F010521 G550 Triticum aestivum cDNA clone G55011C10,
mRNA sequence.

```

Size-fractionated cDNA was precipitated and ligated to HybriZAP arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (PAD-GAL4) was excised from the HybriZAP vector and plasmid DNA isolated."

```

ACCESSION   CD911444
VERSION     CD911444.1  GI:32685768
KEYWORDS
SOURCE      Triticum aestivum (bread wheat)
ORGANISM    Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Poaceae; Triticeae; Triticeae; Triticeae; Triticeae;
            1 (bases 1 to 672)
REFERENCE   1
AUTHORS     Genoplante.
TITLE       Genoplante, a major partnership french program in plant genomics
JOURNAL     Unpublished (2003)
COMMENT     Contact: Genoplante
            Genoplante
            93, rue Henri Rochefort 91025 EVRY CEDEX France
            Tel: 33 1 69 47 54 00
            Fax: 33 1 69 47 54 10
            This sequence has been generated in the framework of the french
            plant genomics programme 'Genoplante' (http://www.genoplante.com)
            and http://genoplante-info.infobiogen.fr.

FEATURES             source
     1..672
     /organism="Triticum aestivum"
     /mol_type="mRNA"
     /cultivar="recital"
     /db_xref="taxon:4565"
     /clone="G55011C10"
     /tissue_type="grain (550 degrees per day after
     pollination)"
     /clone_lib="G550"

ORIGIN
Query Match      33.3%; Score 17; DB 14; Length 672;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      12  TCTTCTTGCTTATCC 28
          |||||
Db      250 TCTTCTTGCTTATCC 266

Search completed: August 2, 2004, 20:27:58
Job time : 2112.71 secs

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GenCore version 5.1.1.6
Copyright (C) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 16:56:38 ; Search time 246.207 Seconds
(without alignments)
879.984 Million cell updates/sec

Title: US-10-068-067-16

Perfect score: 51

Sequence: 1 ggtaccactggtcttcttgt.....caagaacttatcgaataca 51

Scoring table: OLIGO.NUC

Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_29Jan04.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002s.*
- 7: Geneseqn2003as.*
- 8: Geneseqn2003bs.*
- 9: Geneseqn2003cs.*
- 10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	51	100.0	51	6	ABQ78514	Abq78514 Nucleotid
2	51	100.0	51	6	ABQ78519	Abq78519 Nucleotid
3	51	100.0	2895	6	ABQ78513	Abq78513 Nucleotid
4	35	68.6	1193	2	AAT31335	Aat31335 CC-chemok
5	35	68.6	1193	2	AAV07403	Aav07403 Human C-C
6	22	43.1	22	6	ABQ78515	Abq78515 Nucleotid
7	22	43.1	22	6	ABQ78516	Abq78516 Nucleotid
8	22	43.1	22	6	ABQ78521	Abq78521 Nucleotid
9	21	41.2	21	6	ABQ78587	Abq78587 Nucleotid
10	21	41.2	21	6	ABQ78520	Abq78520 Nucleotid
11	21	41.2	21	6	ABQ78517	Abq78517 Nucleotid
12	17	33.3	3140	4	AB112512	Ab112512 Drosophil
13	17	33.3	4400	4	AB112414	Ab112414 Drosophil
14	16	31.4	21	3	AAZ74711	Aaz74711 Human dia
15	16	31.4	265	7	ABX50975	Abx50975 Bovine ES
16	16	31.4	406	9	ADB51450	Adb51450 Primary r
17	16	31.4	586	4	ABA61111	Aba61111 Human foe
18	16	31.4	586	4	AAI41009	Aai41009 Probe #96
19	16	31.4	586	4	AAK35295	Aak35295 Human bon
20	16	31.4	586	4	AAK09404	Aak09404 Human bra
21	16	31.4	586	4	ABS35038	Abs35038 Human liv
22	16	31.4	601	3	AAF11306	Aaf11306 Aspergill
23	16	31.4	661	3	AAF11272	Aaf11272 Aspergill

C	24	16	31.4	823	5	ABV10808	Abv10808 Human pro
C	25	16	31.4	3153	7	ACA54065	Aca54065 Prokaryot
C	26	16	31.4	4563	7	AAD47607	Aad47607 Drosophil
C	27	16	31.4	5532	3	AAA81538	Aaa81538 N. mening
C	28	16	31.4	7967	4	ABL18498	Ab118498 Drosophil
C	29	16	31.4	110000	3	AAAG1489_1	Continuation (2 of
C	30	16	31.4	349980	3	AAF21611_1	Aaf21611 Neisseria
C	31	15	29.4	215	4	AAK79563	Aak79563 Human imm
C	32	15	29.4	240	3	AAAG1159	Aaa61159 SEN virus
C	33	15	29.4	249	6	ABN16387	Abn16387 Human ORF
C	34	15	29.4	278	3	AAA61168	Aaa61168 SEN virus
C	35	15	29.4	388	4	AAI92145	Aai92145 Human pol
C	36	15	29.4	489	2	AAI3914	Aai3914 Enterococ
C	37	15	29.4	489	6	ABS99709	Abs99709 Enterococ
C	38	15	29.4	537	3	AAC94557	Aac94557 Cat flea
C	39	15	29.4	646	3	AAC53290	Aac53290 Arabidops
C	40	15	29.4	700	4	AAH92754	Aah92754 Human inf
C	41	15	29.4	700	4	AAH92753	Aah92753 Human inf
C	42	15	29.4	864	7	ACF70596	Acf70596 Photorhab
C	43	15	29.4	1056	4	ABL25529	Ab125529 Drosophil
C	44	15	29.4	1076	3	AAC45720	Aac45720 Arabidops
C	45	15	29.4	1078	3	AAC41924	Aac41924 Arabidops

ALIGNMENTS

RESULT 1
ABQ78514
ID ABQ78514 standard; DNA; 51 BP.
XX AC ABQ78514;
XX DT 25-NOV-2002 (first entry)
XX DE Nucleotide sequence of a regulatory sequence for human CCR3.
XX KW Human; CC chemokine receptor 3; CCR3; allergic disorder; probe;
XX KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;
XX KW infectious disorder; HIV; respiratory syncytial virus infection; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT misc_binding 24..27
FT FT /*tag= a
FT FT /note= "transcription factor binding site for GATA"
FT FT misc_binding 40..43
FT FT /*tag= b
FT FT /note= "transcription factor binding site for GATA"
XX WO200262848-A2.
XX 15-AUG-2002.
XX PF 06-FEB-2002; 2002WO-US003442.
XX PR 07-FEB-2001; 2001US-0267073P.
XX PR 05-FEB-2002; 2002US-00068067.
XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
XX PI Rothenberg ME, Zimmerman N;
XX DR WPI; 2002-657524/70.
XX New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated
XX exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable
XX of binding to regulatory elements, useful for preventing e.g. allergic
XX inflammatory reactions.

Claim 2; Page 25; 56pp; English.

CC The present sequence represents a probe for the human CC chemokine
 CC receptor 3 (CCR3) gene. The probe comprises +10 to +60 of exon 1 of CCR3,
 CC and is a regulatory sequence for CCR3. CCR3 is expressed on cells
 CC involved in allergic and/or inflammatory disorders. The gene comprises 4
 CC exons, with the coding region present on exon 4. The specification
 CC describes methods of regulating the expression of CCR3. The regulatory
 CC site is derived from an untranslated exon 1, exon 2, exon 3 or promoter
 CC of a human CCR3 gene. Regulating the expression of the chemokine receptor
 CC CCR3 is useful for preventing or treating disorders involving
 CC eosinophils, such as allergic inflammatory and hypersensitivity
 CC reactions, certain types of leukemia, and certain infectious disorders
 CC involving CCR3, e.g. HIV or respiratory syncytial virus infection.
 CC Expression and modulation of CCR3 is a useful tool in assessing
 CC eosinophil targeting and in regulating eosinophil-mediated reactions and
 CC diseases
 XX SQ Sequence 51 BP; 13 A; 12 C; 11 G; 15 T; 0 U; 0 Other;

Query Match 100.0%; Score 51; DB 6; Length 51;
 Best Local Similarity 100.0%; Pred. No. 1.2e-18;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTACCACTGGTCTTCTTGCTTATCCGGCGAAGAACTTATCGAAATACA 51
 Db 1 GGTACCACTGGTCTTCTTGCTTATCCGGCGAAGAACTTATCGAAATACA 51

RESULT 2

ABQ78519
 ID ABQ78519 standard; RNA; 51 BP.

XX AC ABQ78519;

XX DT 25-NOV-2002 (first entry)

XX DE Nucleotide sequence of a regulatory sequence for human CCR3.

XX KW Human; CC chemokine receptor 3; CCR3; allergic disorder; probe;
 KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;
 KW infectious disorder; HIV; respiratory syncytial virus infection; ss.

XX OS Homo sapiens.

XX FN WO200262848-A2.

XX PD 15-AUG-2002.

XX PF 06-FEB-2002; 2002WO-US003442.

XX PR 07-FEB-2001; 2001US-0267073P.

XX PR 05-FEB-2002; 2002US-00068067.

XX PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

XX PI Rothenberg ME, Zimmerman N;

XX DR WPI; 2002-657524/70.

XX PT New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated
 PT exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable
 PT of binding to regulatory elements, useful for preventing e.g. allergic
 PT inflammatory reactions.

XX PS Claim 7; Page 56; 56pp; English.

XX CC The present sequence represents a probe for the human CC chemokine
 CC receptor 3 (CCR3) gene. The probe is a regulatory sequence for CCR3. CCR3
 CC is expressed on cells involved in allergic and/or inflammatory disorders.
 CC The gene comprises 4 exons, with the coding region present on exon 4. The
 CC specification describes methods of regulating the expression of CCR3. The
 CC regulatory site is derived from an untranslated exon 1, exon 2, exon 3 or
 CC promoter of a human CCR3 gene. Regulating the expression of the chemokine
 CC receptor CCR3 is useful for preventing or treating disorders involving

CC eosinophils, such as allergic inflammatory and hypersensitivity
 CC reactions, certain types of leukemia, and certain infectious disorders
 CC involving CCR3, e.g. HIV or respiratory syncytial virus infection.
 CC Expression and modulation of CCR3 is a useful tool in assessing
 CC eosinophil targeting and in regulating eosinophil-mediated reactions and
 CC diseases

XX SQ Sequence 51 BP; 13 A; 12 C; 11 G; 0 T; 15 U; 0 Other;

Query Match 100.0%; Score 51; DB 6; Length 51;
 Best Local Similarity 70.6%; Pred. No. 1.2e-18;
 Matches 36; Conservative 15; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTACCACTGGTCTTCTTGCTTATCCGGCGAAGAACTTATCGAAATACA 51
 Db 1 GGUACCAUGGUCUUCUGUGCUUACCGGCGAAGAACTTATCGAAATACA 51

RESULT 3

ABQ78513
 ID ABQ78513 standard; DNA; 2895 BP.

XX AC ABQ78513;

XX DT 25-NOV-2002 (first entry)

XX DE Nucleotide sequence of the human CCR3 gene promoter.

XX KW Human; CC chemokine receptor 3; CCR3; allergic disorder;
 KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;
 KW infectious disorder; HIV; respiratory syncytial virus infection;
 KW promoter; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 FT misc_signal 1640..1645
 FT /tag= a
 FT /note= "splice donor consensus site"

XX FN WO200262848-A2.

XX PD 15-AUG-2002.

XX PF 06-FEB-2002; 2002WO-US003442.

XX PR 07-FEB-2001; 2001US-0267073P.

XX PR 05-FEB-2002; 2002US-00068067.

XX PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

XX PI Rothenberg ME, Zimmerman N;

XX DR WPI; 2002-657524/70.

XX PT New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated
 PT exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable
 PT of binding to regulatory elements, useful for preventing e.g. allergic
 PT inflammatory reactions.

XX PS Disclosure; Fig 4; 56pp; English.

XX CC The present sequence represents the promoter of the human CC chemokine
 CC receptor 3 (CCR3) gene. CCR3 is expressed on cells involved in allergic
 CC and/or inflammatory disorders. The gene comprises 4 exons, with the
 CC coding region present on exon 4. The specification describes methods of
 CC regulating the expression of CCR3. The regulatory site is derived from an
 CC untranslated exon 1, exon 2, exon 3 or promoter of a human CCR3 gene.
 CC Regulating the expression of the chemokine receptor CCR3 is useful for
 CC preventing or treating disorders involving eosinophils, such as allergic
 CC inflammatory and hypersensitivity reactions, certain types of leukemia,
 CC and certain infectious disorders involving CCR3, e.g. HIV or respiratory
 CC syncytial virus infection. Expression and modulation of CCR3 is a useful

CC tool in assessing eosinophil targeting and in regulating eosinophil-mediated reactions and diseases

SQ Sequence 2895 BP; 829 A; 556 G; 920 T; 0 U; 0 Other;

Query Match 100.0%; Score 51; DB 6; Length 2895;
Best Local Similarity 100.0%; Pred. No. 1.3e-18;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACCACTGGTCTTCTTGTGCTTATCCGGCAGAACTTATCGAAATACA 51
|||||
DB 1561 GGTACCACTGGTCTTCTTGTGCTTATCCGGCAGAACTTATCGAAATACA 1611

RESULT 4

AAT31335

ID AAT31335 standard; cDNA; 1193 BP.

XX

AC AAT31335;

XX

DT 15-NOV-1996 (first entry)

XX

DE CC-chemokine receptor 3 cDNA clone.

XX

KW CC-chemokine receptor 3; CX3-3; Eos-L2; inhibitor; antisense;
ant inflammatory; eosinophil; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

XX

CDS 92..1159

FT

/*tag= a

FT

variation 918..919

FT

/*tag= b

FT

/*note= "CCR-3 cDNA clone has GC at positions 918-919,
coding for serine (AGC) at position 276; a genomic clone
has CG at these positions, coding for threonine (AGC)"

FT

XX

PN W09622371-A2.

XX

XX 25-JUL-1996.

XX

XX 19-JAN-1996; 96WO-US000608.

XX

XX 19-JAN-1995; 95US-00375199.

XX

(LEUK-) LEUKOSITE INC.

PA

PA (BGM) BRIGHAM & WOMENS HOSPITAL.

XX

XX (CHIL-) CHILDRENS MEDICAL CENT.

XX

PI Gerard CJ, Gerard NP, Mackay CR, Ponath PD, Post TW, Qin S;

XX

DR WPI; 1996-354528/35.

XX

DR P-PSDB; AAW03377.

XX

PT Mammalian chemokine receptor-3 and related nucleic acids - useful to
identify receptor inhibitors to treat inflammatory disease, e.g.

XX

PT autoimmune disorders, certain cancers, etc.

XX

PS Claim 1; Page 111-113; 153pp; English.

XX

CC A genomic DNA clone (AAT31335) codes for a novel receptor (AAW03377),
designated Eos L2 or C-C chemokine receptor 3 (CCR-3), involved in
leukocyte migration associated with inflammation. It was isolated from a
human library constructed from eosinophils obtd. from a patient with
hyper-eosinophilic syndrome using a probe (p4 cDNA) encoding the MIP-
1alpha/RANTES receptor. A CCR-3 genomic clone (AAT31334) was also
isolated, and a consensus sequence is given in AAT31336. The cDNA and
genomic clones can be used for the prodn. of recombinant CCR-3 in host
cells, or to design antisense sequences useful for treating inflammatory
disease

XX

SQ Sequence 1193 BP; 274 A; 310 C; 275 G; 334 T; 0 U; 0 Other;

Query Match 68.6%; Score 35; DB 2; Length 1193;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TTGTGCTTATCCGGCAGAACTTATCGAAATACA 51
|||||
DB 1 TTGTGCTTATCCGGCAGAACTTATCGAAATACA 35

RESULT 5

AAV07403

ID AAV07403 standard; cDNA; 1193 BP.

XX

AC AAV07403;

XX

DT 28-SEP-1998 (first entry)

XX

DE Human C-C chemokine receptor 3 cDNA.

XX

KW C-C chemokine receptor 3; CCR3; CCR3; Eos L2; human;
G protein-coupled receptor; leukocyte; antibody; antagonist;
inflammation; allergy; asthma; graft rejection; infection;
autoimmune disease; drug screening; therapy; ds.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

XX

CDS 92..1159

FT

/*tag= a

FT

PN W09814480-A1.

XX

XX 09-APR-1998.

XX

XX 24-SEP-1997; 97WO-US017103.

XX

XX 30-SEP-1996; 96US-00720565.

XX

(LEUK-) LEUKOSITE INC.

XX

XX Mackay CR, Ponath PD;

XX

XX WPI; 1998-286418/25.

XX

XX P-PSDB; AAW51745.

XX

Antibodies to chemokine receptor-3 protein - useful for diagnosis and
treatment of inflammatory conditions, e.g. allergy, asthma, autoimmune
disease, graft rejection or cancer.

XX

PS Example 8; Page 134-136; 185pp; English.

XX

This cDNA codes for novel human C-C chemokine receptor 3 (see AAW51745),
also designated CCR-3, CCR3 or Eos L2, that binds and mediates chemotaxis
in response to chemokines such as eotaxin, RANTES and MCP-3. The cDNA was
isolated from a human eosinophil cDNA library constructed from
eosinophils obtained from a patient with hyperesinophilic syndrome, and
using CCR-1 cDNA as probe. A genomic DNA sequence (see AAV07402) is also
provided as well as a consensus sequence (see AAV07404) for CCR-3. The
invention relates to isolated and/or recombinant nucleic acids encoding
CCR-3, isolated or recombinant CCR-3 polypeptides, recombinant nucleic
acid constructs, host cells useful for production of recombinant CCR-3
proteins, to antibodies reactive with the receptors, and to methods of
using these products to identify ligands, antagonists and agonists of
receptor function. Inhibitors of CCR-3 can be used to treat: inflammatory
or allergic diseases and conditions, including respiratory allergic
diseases such as asthma, allergic rhinitis, hypersensitivity lung
disease, hypersensitivity pneumonitis, eosinophilic pneumonia (e.g.
Loeffler's syndrome, chronic eosinophilic pneumonia, interstitial lung
disease (ILD) e.g. idiopathic pulmonary fibrosis or ILD associated with
rheumatoid arthritis, systemic lupus erythematosus, ankylosing
spondylitis, systemic sclerosis, Sjogren's syndrome, polymyositis or
dermatomyositis), systemic anaphylaxis or hypersensitivity responses,

CC drug allergy, insect sting allergy, inflammatory bowel disease, such as
 CC Crohn's disease and ulcerative colitis, spondylarthropathy, scleroderma,
 CC psoriasis, inflammatory dermatosis such as dermatitis, eczema, atopic
 CC dermatitis, allergic contact dermatitis, urticaria, vasculitis (e.g.
 CC necrotizing, cutaneous and hypersensitivity vasculitis); eosinophilic
 CC myositis and eosinophilic fasciitis; autoimmune diseases such as
 CC rheumatoid arthritis, psoriatic arthritis, multiple sclerosis, systemic
 CC lupus erythematosus, myasthenia gravis, juvenile onset diabetes,
 CC glomerulonephritis, autoimmune thyroiditis and Behcet's disease; graft
 CC rejection, including allograft rejection or graft-versus-host disease;
 CC cancers with leukocyte infiltration of the skin or organs; and also
 CC reperfusion injury, atherosclerosis, certain haematologic malignancies,
 CC septic shock and endotoxic shock. Promoters of CCR-3 function can be used
 CC for treating: immunosuppression e.g. in AIDS patients or individuals
 CC undergoing radiation therapy, chemotherapy, therapy for autoimmune
 CC disease or other drug therapy, and immunosuppression due congenital
 CC deficiency in receptor function or other causes; and infectious diseases
 CC such as parasitic diseases, including Helminth infections, such as
 CC nematodes (round worms). The agents can also be used for detection and
 CC diagnosis
 XX
 SQ Sequence 1193 BP; 274 A; 310 C; 275 G; 334 T; 0 U; 0 Other;

Query Match 58.6%; Score 35; DB 2; Length 1193;
 Best Local Similarity 100.0%; Pred. No. 1.1e-09;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TTGTGCTTATCCGGGCAAGAACTTATCGAATACA 51
 DB 1 TTGTGCTTATCCGGGCAAGAACTTATCGAATACA 35

RESULT 6
 ABQ78515
 ID ABQ78515 standard; DNA; 22 BP.
 XX
 AC ABQ78515;
 XX
 XX 25-NOV-2002 (first entry)
 DT
 XX
 DE Nucleotide sequence of a regulatory sequence for human CCR3.
 XX
 KW Human; CC chemokine receptor 3; CCR3; allergic disorder; probe;
 KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;
 KW infectious disorder; HIV; respiratory syncytial virus infection; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200262848-A2.
 XX
 PD 15-AUG-2002.
 XX
 PF 06-FEB-2002; 2002WO-US003442.
 XX
 PR 07-FEB-2001; 2001US-0267073P.
 PR 05-FEB-2002; 2002US-00068067.
 XX
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 XX
 PI Rothenberg ME, Zimmerman N;
 XX
 DR WPI; 2002-657524/70.

PT New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated
 PT exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable
 PT of binding to regulatory elements, useful for preventing e.g. allergic
 PT inflammatory reactions.
 XX
 XX Claim 6; Page 54; 56pp; English.
 XX
 XX The present sequence represents a probe for the human CC chemokine
 CC receptor 3 (CCR3) gene. The probe is a regulatory sequence for CCR3. CCR3
 CC is expressed on cells involved in allergic and/or inflammatory disorders.
 CC The gene comprises 4 exons, with the coding region present on exon 4. The
 CC specification describes methods of regulating the expression of CCR3. The
 CC regulatory site is derived from an untranslated exon 1, exon 2, exon 3 or
 CC promoter of a human CCR3 gene. Regulating the expression of the chemokine
 CC receptor CCR3 is useful for preventing or treating disorders involving
 CC eosinophils, such as allergic inflammatory and hypersensitivity
 CC reactions, certain types of leukemia, and certain infectious disorders
 CC involving CCR3, e.g. HIV or respiratory syncytial virus infection.
 CC Expression and modulation of CCR3 is a useful tool in assessing

CC The gene comprises 4 exons, with the coding region present on exon 4. The
 CC specification describes methods of regulating the expression of CCR3. The
 CC regulatory site is derived from an untranslated exon 1, exon 2, exon 3 or
 CC promoter of a human CCR3 gene. Regulating the expression of the chemokine
 CC receptor CCR3 is useful for preventing or treating disorders involving
 CC eosinophils, such as allergic inflammatory and hypersensitivity
 CC reactions, certain types of leukemia, and certain infectious disorders
 CC involving CCR3, e.g. HIV or respiratory syncytial virus infection.
 CC Expression and modulation of CCR3 is a useful tool in assessing
 CC eosinophil targeting and in regulating eosinophil-mediated reactions and
 CC diseases
 XX

SQ Sequence 22 BP; 2 A; 6 C; 6 G; 8 T; 0 U; 0 Other;

Query Match 43.1%; Score 22; DB 6; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.018;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACCACTGCTCTTCTTGTC 22
 DB 1 GGTACCACTGCTCTTCTTGTC 22

RESULT 7
 ABQ78516
 ID ABQ78516 standard; DNA; 22 BP.
 XX
 AC ABQ78516;
 XX
 XX 25-NOV-2002 (first entry)
 DT
 XX
 DE Nucleotide sequence of a regulatory sequence for human CCR3.
 XX
 KW Human; CC chemokine receptor 3; CCR3; allergic disorder; probe;
 KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;
 KW infectious disorder; HIV; respiratory syncytial virus infection; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200262848-A2.
 XX
 PD 15-AUG-2002.
 XX
 PF 06-FEB-2002; 2002WO-US003442.
 XX
 PR 07-FEB-2001; 2001US-0267073P.
 PR 05-FEB-2002; 2002US-00068067.
 XX
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 XX
 PI Rothenberg ME, Zimmerman N;
 XX
 DR WPI; 2002-657524/70.

PT New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated
 PT exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable
 PT of binding to regulatory elements, useful for preventing e.g. allergic
 PT inflammatory reactions.
 XX
 XX Claim 6; Page 54; 56pp; English.
 XX
 XX The present sequence represents a probe for the human CC chemokine
 CC receptor 3 (CCR3) gene. The probe is a regulatory sequence for CCR3. CCR3
 CC is expressed on cells involved in allergic and/or inflammatory disorders.
 CC The gene comprises 4 exons, with the coding region present on exon 4. The
 CC specification describes methods of regulating the expression of CCR3. The
 CC regulatory site is derived from an untranslated exon 1, exon 2, exon 3 or
 CC promoter of a human CCR3 gene. Regulating the expression of the chemokine
 CC receptor CCR3 is useful for preventing or treating disorders involving
 CC eosinophils, such as allergic inflammatory and hypersensitivity
 CC reactions, certain types of leukemia, and certain infectious disorders
 CC involving CCR3, e.g. HIV or respiratory syncytial virus infection.
 CC Expression and modulation of CCR3 is a useful tool in assessing

CC eosinophil targeting and in regulating eosinophil-mediated reactions and
CC diseases
XX
SQ Sequence 22 BP; 5 A; 5 C; 6 G; 6 T; 0 U; 0 Other;
Query Match 43.1%; Score 22; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 CTTGTGCTTATCCGGCAAGAA 37
DB 1 CTTGTGCTTATCCGGCAAGAA 22
RESULT 8
ABQ78521
ID ABQ78521 standard; RNA; 22 BP.
XX
AC ABQ78521;
XX
DT 25-NOV-2002 (first entry)
XX
DE Nucleotide sequence of a regulatory sequence for human CCR3.
XX
KW Human; CC chemokine receptor 3; CCR3; allergic disorder; probe;
KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;
KW infectious disorder; HIV; respiratory syncytial virus infection; ss.
XX
OS Homo sapiens.
XX
PN WO200262848-A2.
XX
PD 15-AUG-2002.
XX
PF 06-FEB-2002; 2002WO-US003442.
XX
PR 07-FEB-2001; 2001US-0267073P.
XX
PR 05-FEB-2002; 2002US-00068067.
XX
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
XX
PI Rothenberg ME, Zimmerman N;
XX
DR WPI; 2002-657524/70.
XX
PT New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated
PT exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable
PT of binding to regulatory elements, useful for preventing e.g. allergic
PT inflammatory reactions.
XX
PS Claim 8; Page 56; 56pp; English.
XX
CC The present sequence represents a probe for the human CC chemokine
CC receptor 3 (CCR3) gene. The probe is a regulatory sequence for CCR3. CCR3
CC is expressed on cells involved in allergic and/or inflammatory disorders.
CC The gene comprises 4 exons, with the coding region present on exon 4. The
CC specification describes methods of regulating the expression of CCR3. The
CC regulatory site is derived from an untranslated exon 1, exon 2, exon 3 or
CC promoter of a human CCR3 gene. Regulating the expression of the chemokine
CC receptor CCR3 is useful for preventing or treating disorders involving
CC eosinophils, such as allergic inflammation and hypersensitivity
CC reactions, certain types of leukemia, and certain infectious disorders
CC involving CCR3, e.g. HIV or respiratory syncytial virus infection.
CC Expression and modulation of CCR3 is a useful tool in assessing
CC eosinophil targeting and in regulating eosinophil-mediated reactions and
CC diseases
XX
SQ Sequence 22 BP; 5 A; 5 C; 6 G; 6 T; 6 U; 0 Other;
Query Match 43.1%; Score 22; DB 6; Length 22;
Best Local Similarity 72.7%; Pred. No. 0.018;
Matches 16; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 16 CTTGTGCTTATCCGGCAAGAA 37
DB 1 CUUGUCUUAUCCGGCAAGAA 22
RESULT 9
ABQ78587
ID ABQ78587 standard; RNA; 21 BP.
XX
AC ABQ78587;
XX
DT 25-NOV-2002 (first entry)
XX
DE Nucleotide sequence of a regulatory sequence for human CCR3.
XX
KW Human; CC chemokine receptor 3; CCR3; allergic disorder; probe;
KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;
KW infectious disorder; HIV; respiratory syncytial virus infection; ss.
XX
OS Homo sapiens.
XX
PN WO200262848-A2.
XX
PD 15-AUG-2002.
XX
PF 06-FEB-2002; 2002WO-US003442.
XX
PR 07-FEB-2001; 2001US-0267073P.
XX
PR 05-FEB-2002; 2002US-00068067.
XX
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
XX
PI Rothenberg ME, Zimmerman N;
XX
DR WPI; 2002-657524/70.
XX
PT New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated
PT exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable
PT of binding to regulatory elements, useful for preventing e.g. allergic
PT inflammatory reactions.
XX
PS Claim 8; Page 56; 56pp; English.
XX
CC The present sequence represents a probe for the human CC chemokine
CC receptor 3 (CCR3) gene. The probe is a regulatory sequence for CCR3. CCR3
CC is expressed on cells involved in allergic and/or inflammatory disorders.
CC The gene comprises 4 exons, with the coding region present on exon 4. The
CC specification describes methods of regulating the expression of CCR3. The
CC regulatory site is derived from an untranslated exon 1, exon 2, exon 3 or
CC promoter of a human CCR3 gene. Regulating the expression of the chemokine
CC receptor CCR3 is useful for preventing or treating disorders involving
CC eosinophils, such as allergic inflammation and hypersensitivity
CC reactions, certain types of leukemia, and certain infectious disorders
CC involving CCR3, e.g. HIV or respiratory syncytial virus infection.
CC Expression and modulation of CCR3 is a useful tool in assessing
CC eosinophil targeting and in regulating eosinophil-mediated reactions and
CC diseases
XX
SQ Sequence 21 BP; 10 A; 4 C; 3 G; 0 T; 4 U; 0 Other;
Query Match 41.2%; Score 21; DB 6; Length 21;
Best Local Similarity 81.0%; Pred. No. 0.066;
Matches 17; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 31 GCAAGAACTTATCGAATAACA 51
DB 1 GCAAGAACTTATCGAATAACA 21
RESULT 10
ABQ78520
ID ABQ78520 standard; RNA; 21 BP.
XX

```

AC ABQ78520;
XX
DT 25-NOV-2002 (first entry)
XX
DE Nucleotide sequence of a regulatory sequence for human CCR3.
XX
KW Human; CC chemokine receptor 3; CCR3; allergic disorder; probe;
KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;
KW infectious disorder; HIV; respiratory syncytial virus infection; ss.
XX
OS Homo sapiens.
XX
FN WO200262848-A2.
XX
PD 15-AUG-2002.
XX
PF 06-FEB-2002; 2002WO-US003442.
XX
PR 07-FEB-2001; 2001US-0267073P.
XX
PR 05-FEB-2002; 2002US-00068067.
XX
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
XX
PI Rothenberg ME, Zimmerman N;
XX
DR WPI; 2002-657524/70.
XX
XX New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated
PT exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable
PT of binding to regulatory elements, useful for preventing e.g. allergic
PT inflammatory reactions.
XX
PS Claim 8; Page 56; 56pp; English.
XX
CC The present sequence represents a probe for the human CC chemokine
CC receptor 3 (CCR3) gene. The probe is a regulatory sequence for CCR3. CCR3
CC is expressed on cells involved in allergic and/or inflammatory disorders.
CC The gene comprises 4 exons, with the coding region present on exon 4. The
CC specification describes methods of regulating the expression of CCR3. The
CC regulatory site is derived from an untranslated exon 1, exon 2, exon 3 or
CC promoter of a human CCR3 gene. Regulating the expression of the chemokine
CC receptor CCR3 is useful for preventing or treating disorders involving
CC eosinophils, such as allergic inflammatory and hypersensitivity
CC reactions, certain types of leukemia, and certain infectious disorders
CC involving CCR3, e.g. HIV or respiratory syncytial virus infection.
CC Expression and modulation of CCR3 is a useful tool in assessing
CC eosinophil targeting and in regulating eosinophil-mediated reactions and
CC diseases
XX
SQ Sequence 21 BP; 2 A; 5 C; 6 G; 0 T; 8 U; 0 Other;
Query Match 41.2%; Score 21; DB 6; Length 21;
Best Local Similarity 61.9%; Pred. No. 0.066;
Matches 13; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACCACTGGTCTCTGTG 21
Dd 1 GGUACACUGGUCUCUGUG 21

RESULT 11
ABQ78517
ID ABQ78517 standard; DNA; 21 BP.
XX
AC ABQ78517;
XX
DT 25-NOV-2002 (first entry)
XX
DE Nucleotide sequence of a regulatory sequence for human CCR3.
XX
KW Human; CC chemokine receptor 3; CCR3; allergic disorder; probe;
KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;
KW infectious disorder; HIV; respiratory syncytial virus infection; ss.
XX
OS Homo sapiens.
XX
FN WO200262848-A2.
XX
PD 15-AUG-2002.
XX
PF 06-FEB-2002; 2002WO-US003442.
XX
PR 07-FEB-2001; 2001US-0267073P.
XX
PR 05-FEB-2002; 2002US-00068067.
XX
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
XX
PI Rothenberg ME, Zimmerman N;
XX
DR WPI; 2002-657524/70.
XX
XX New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated
PT exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable
PT of binding to regulatory elements, useful for preventing e.g. allergic
PT inflammatory reactions.
XX
PS Claim 8; Page 56; 56pp; English.
XX
CC The present sequence represents a probe for the human CC chemokine
CC receptor 3 (CCR3) gene. The probe is a regulatory sequence for CCR3. CCR3
CC is expressed on cells involved in allergic and/or inflammatory disorders.
CC The gene comprises 4 exons, with the coding region present on exon 4. The
CC specification describes methods of regulating the expression of CCR3. The
CC regulatory site is derived from an untranslated exon 1, exon 2, exon 3 or
CC promoter of a human CCR3 gene. Regulating the expression of the chemokine
CC receptor CCR3 is useful for preventing or treating disorders involving
CC eosinophils, such as allergic inflammatory and hypersensitivity
CC reactions, certain types of leukemia, and certain infectious disorders
CC involving CCR3, e.g. HIV or respiratory syncytial virus infection.
CC Expression and modulation of CCR3 is a useful tool in assessing
CC eosinophil targeting and in regulating eosinophil-mediated reactions and
CC diseases
XX
SQ Sequence 21 BP; 2 A; 5 C; 6 G; 0 T; 8 U; 0 Other;
Query Match 41.2%; Score 21; DB 6; Length 21;
Best Local Similarity 61.9%; Pred. No. 0.066;
Matches 13; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACCACTGGTCTCTGTG 21
Dd 1 GGUACACUGGUCUCUGUG 21

RESULT 12
ABQ78512/c
ID ABQ78512 standard; cDNA; 3140 BP.
XX
AC ABQ78512;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 32018.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
FN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
XX

```

PR 11-JUL-2000; 2000US-00614150.
XX (PEKE) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
DR P-PSDB; ABB69409.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
XX Claim 1; SEQ ID NO 32019; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-
CC ABBS72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 3140 BP; 789 A; 738 C; 769 G; 844 T; 0 U; 0 Other;
SQ
Query Match 33.3%; Score 17; DB 4; Length 3140;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 33 AAGAACTTATCGAAATA 49
DB 2243 AAGAACTTATCGAAATA 2227
RESULT 13
ID ABL12414/c
XX ABL12414 standard; cDNA; 4400 BP.
XX
XX ABL12414;
XX
XX 26-MAR-2002 (first entry)
XX
XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 31724.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
XX Drosophila melanogaster.
OS
XX WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US009231.
XX
XX 23-MAR-2000; 2000US-0191637P.
PR
XX 11-JUL-2000; 2000US-00614150.
XX
XX (PEKE) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
DR P-PSDB; ABB68311.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
XX Claim 1; SEQ ID NO 31724; 21pp + Sequence Listing; English.
PS

XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-
CC ABBS72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 4400 BP; 1037 A; 1066 C; 1109 G; 1188 T; 0 U; 0 Other;
SQ
Query Match 33.3%; Score 17; DB 4; Length 4400;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 33 AAGAACTTATCGAAATA 49
DB 765 AAGAACTTATCGAAATA 749
RESULT 14
ID AAZ74711
XX AAZ74711 standard; DNA; 21 BP.
XX
XX AAZ74711;
XX
XX 10-SEP-2001 (first entry)
XX
XX Human biallelic marker downstream amplification primer SEQ ID NO:9067.
XX
XX Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
XX Homo sapiens.
OS
XX WO9954500-A2.
XX
XX 28-OCT-1999.
XX
XX 21-APR-1999; 99WO-IB000822.
XX
XX 21-APR-1998; 98US-0082614P.
PR
XX 23-NOV-1998; 98US-0109732P.
XX
XX (GEST) GENSET.
XX
XX Cohen D, Blumenfeld M, Chumakov I;
XX WPI; 2000-013267/01.
XX
XX Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
XX Claim 8; Page 2164; 2745pp; English.
XX
XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC

CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
 CC 3367, are not actually given a sequence in the Sequence Listing from the
 CC Present invention

XX SQ Sequence 21 BP; 4 A; 4 C; 5 G; 8 T; 0 U; 0 Other;
 Query Match 31.4%; Score 16; DB 3; Length 21;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 10 GGTCTCTTGTGCTTA 25
 Db 1 GGTCTCTTGTGCTTA 16
 |||||

RESULT 15
 ABX50975/c
 ID ABX50975 standard; cDNA; 265 BP.

XX AC ABX50975;

XX 25-FEB-2003 (first entry)

XX DE Bovine EST associated with lactation/muscle/fat deposition #904.

XX KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
 KW muscle deposition; fat deposition; genome mapping; gene identification;
 KW gene analysis; cattle breeding.

XX OS Bos Taurus.

XX PN US2002137160-A1.

XX PD 26-SEP-2002.

XX PF 26-OCT-2001; 2001US-00983965.

XX PR 17-DEC-1998; 98US-0113678P.

XX PR 15-DEC-1999; 99US-00465231.

XX PA (BYAT/) BYATT J C.

XX PA (MATH/) MATHIALAGAN N.

XX PA (TAON/) TAO N.

XX PA (WARR/) WARREN W C.

XX PI Byatt JC, Mathialagan N, Tao N, Warren WC;

XX DR WPI; 2003-102386/09.

XX PT Purified nucleic acid molecules, useful for genome mapping, gene
 PT identification and analysis, cattle breeding or preparation of constructs
 PT for cattle gene expression and genetically improved cattle.

XX PS Claim 2; SEQ ID NO 904; 38pp; English.

XX The invention relates to a purified nucleic acid molecule associated with
 CC lactation or muscle and fat deposition (designated LMFD), derived from
 CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
 CC nucleic acid molecule comprising any of 5912 nucleotide sequences,
 CC appearing as ABX50072-ABX55983, or complements of them. Also included are
 CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
 CC acid linked to a promoter and a 3' non- translated sequence that
 CC functions in the cell to cause termination of transcription and addition
 CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
 CC (2) determining a level or pattern of a molecule in a bovine cell or
 CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
 CC of the 5912 nucleic acid sequences or its complement or fragment) with a
 CC complementary nucleic acid molecule obtained from the bovine cell or
 CC tissue, where hybridisation between the marker nucleic acid and the
 CC complementary nucleic acid permits the detection of the molecule; and
 CC detecting the level or pattern of the complementary nucleic acid, where
 CC the detection of the complementary nucleic acid is predictive of the
 CC level or pattern of the molecule. The LMFD nucleic acid is used for

CC determining a level or pattern of a molecule in a bovine cell or tissue.
 CC It is useful for genome mapping, gene identification and analysis, cattle
 CC breeding, preparation of constructs for use in cattle gene expression, or
 CC for genetically improving cattle. The present sequence is one of the 5912
 CC bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The present
 CC sequence was not shown in the specification but was obtained in
 CC electronic format from the USPTO web site:
 CC seqdata.uspto.gov/sequence.html?DocID=20020137160

XX SQ Sequence 265 BP; 67 A; 72 C; 67 G; 59 T; 0 U; 0 Other;

Query Match 31.4%; Score 16; DB 7; Length 265;

Best Local Similarity 100.0%; Pred. No. 42;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 16 CTTGTGCTTATCCGGG 31

Db 217 CTTGTGCTTATCCGGG 202

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Search completed: August 2, 2004, 18:24:21
 Job time : 249.207 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 16:56:11 ; Search time 248 Seconds
(without alignments)
1008.307 Million cell updates/sec

Title: US-10-068-067-16

Perfect score: 51

Sequence: 1 ggtaccactggtctcttgttgc.....caagaacttatcgaaataca 51

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3222919 seqs, 2451570024 residues

Total number of hits satisfying chosen parameters: 6445838

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq**
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6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq**
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14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq**
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18: /cgn2_6/ptodata/1/pubpna/US40_NEW_PUB.seq**
19: /cgn2_6/ptodata/1/pubpna/US40_PUBCOMB.seq**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	51	14	US-10-068-067-16
2	51	100.0	51	14	Sequence 16, Appl
3	51	100.0	2895	14	Sequence 21, Appl
4	35	68.6	1193	15	Sequence 11, Appl
5	26	51.0	394	13	US-10-085-783A-39054
6	26	51.0	396	16	Sequence 39054, A
7	25	49.0	396	13	US-10-085-783A-38805
8	25	49.0	396	16	Sequence 38805, A
9	24.4	47.8	669	13	US-10-027-632-201530
10	24.4	47.8	669	16	Sequence 201530, A
11	24.4	47.8	1312	13	US-10-027-632-201531
12	24.4	47.8	1312	16	Sequence 201531, A
13	23.4	45.9	611	13	US-10-027-632-214974
14	23.4	45.9	611	16	Sequence 214974, A

15	23.4	45.9	1327	17	US-10-437-963-20957	Sequence 20957, A
16	23.4	45.9	1349	13	US-10-027-632-251334	Sequence 251334, A
17	23.4	45.9	1349	16	US-10-027-632-251334	Sequence 251334, A
18	22.6	44.3	1135	13	US-10-424-599-18358	Sequence 18358, A
19	22.4	43.9	565	13	US-10-027-632-128025	Sequence 128025, A
20	22.4	43.9	565	16	US-10-027-632-128025	Sequence 128025, A
21	22.4	43.9	576	13	US-10-027-632-256503	Sequence 256503, A
22	22.4	43.9	576	13	US-10-027-632-256504	Sequence 256504, A
23	22.4	43.9	576	16	US-10-027-632-256503	Sequence 256503, A
24	22.4	43.9	576	16	US-10-027-632-256504	Sequence 256504, A
25	22.4	43.9	584	13	US-10-027-632-131371	Sequence 131371, A
26	22.4	43.9	584	16	US-10-027-632-131371	Sequence 131371, A
27	22.4	43.9	1343	15	US-10-078-770-115	Sequence 115, App
28	22.4	43.9	1343	15	US-10-078-770-115	Sequence 115, App
29	22.4	43.9	1372	13	US-10-425-114-17357	Sequence 17357, A
30	22.4	43.9	2170	13	US-10-425-114-24889	Sequence 24889, A
31	22.4	43.9	2277	13	US-10-425-114-15509	Sequence 15509, A
32	22.2	43.5	1719	9	US-09-974-300-648	Sequence 648, App
33	22.2	43.5	1861	9	US-09-822-830A-4	Sequence 4, Appl
34	22.2	43.5	2000	16	US-10-260-238-2606	Sequence 268, App
35	22.2	43.5	2102	9	US-09-764-864-268	Sequence 167, App
36	22.2	43.5	2784	9	US-09-764-864-167	Sequence 1025, App
37	22.2	43.5	3050	13	US-10-087-192-1025	Sequence 1024, App
38	22.2	43.5	60500	13	US-10-087-192-1024	Sequence 17, Appl
39	22	43.1	22	14	US-10-068-067-17	Sequence 18, Appl
40	22	43.1	22	14	US-10-068-067-18	Sequence 23, Appl
41	22	43.1	22	14	US-10-085-783A-38234	Sequence 38234, A
42	22	43.1	467	13	US-10-242-535A-38234	Sequence 38234, A
43	22	43.1	467	16	US-10-242-535A-38234	Sequence 217, App
44	22	43.1	92880	12	US-09-997-722-217	Sequence 7, Appl
45	21.8	42.7	80462	17	US-10-322-281-7	

ALIGNMENTS

RESULT 1

US-10-068-067-16
; Sequence 16, Application US/10068067
; Publication No. US20020151064A1
; GENERAL INFORMATION:
; APPLICANT: Rothenberg, Marc E.
; APPLICANT: Zimmermann, Nives
; APPLICANT: Children's Hospital Medical Center
; TITLE OF INVENTION: REGULATION OF CCR3 EXPRESSION
; FILE REFERENCE: CMC-153
; CURRENT APPLICATION NUMBER: US/10/068,067
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 60/267,073
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-068-067-16

Query Match 100.0%; Score 51; DB 14; Length 51;
Best Local Similarity 100.0%; Pred.No. 9.4e-12;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGTACCACTGGTCTCTTGTGCTTATCCGGGCAAGAACTTATCGAAATACA 51
Db 1 GGTACCACTGGTCTCTTGTGCTTATCCGGGCAAGAACTTATCGAAATACA 51

RESULT 2

US-10-068-067-21
; Sequence 21, Application US/10068067
; Publication No. US20020151064A1
; GENERAL INFORMATION:
; APPLICANT: Rothenberg, Marc E.

APPLICANT: Zimmermann, Nives
TITLE OF INVENTION: Children's Hospital Medical Center
FILE REFERENCE: CMC-153
CURRENT APPLICATION NUMBER: US/10/068,067
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: 60/267,073
PRIOR FILING DATE: 2001-02-07
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.1
SEQ ID NO 21
LENGTH: 51
TYPE: RNA
ORGANISM: Homo sapiens
US-10-068-067-21

Query Match 100.0%; Score 51; DB 14; Length 51;
Best Local Similarity 70.6%; Pred. No. 9.4e-12;
Matches 36; Conservative 15; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTACCACTGGTCTTCTGTGCTTATCCGGGCAAGAACTTATCGAAATACA 51
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Db 1 GGUACCACUGGUCUUCUGUGCUUAUCCGGGCAAGAACTTATCGAAATACA 51

RESULT 3
US-10-068-067-11
Sequence 11, Application US/10068067
Publication No. US20020151064A1
GENERAL INFORMATION:
APPLICANT: Rothenberg, Marc E.
APPLICANT: Zimmermann, Nives
TITLE OF INVENTION: REGULATION OF CCR3 EXPRESSION
FILE REFERENCE: CMC-153
CURRENT APPLICATION NUMBER: US/10/068,067
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: 60/267,073
PRIOR FILING DATE: 2001-02-07
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 2895
TYPE: DNA
ORGANISM: Homo sapiens
US-10-068-067-11

Query Match 100.0%; Score 51; DB 14; Length 2895;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTACCACTGGTCTTCTGTGCTTATCCGGGCAAGAACTTATCGAAATACA 51
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Db 1561 GGTACCACTGGTCTTCTGTGCTTATCCGGGCAAGAACTTATCGAAATACA 1611

RESULT 4
US-10-283-028-3
Sequence 3, Application US/10283028
Publication No. US20030143684A1
GENERAL INFORMATION:
APPLICANT: Gerard, Craig J.
Gerard, No. US20030143684A1ma P.
Mackay, Charles R.
Ponath, Paul D.
Post, Theodore W.
Qin, Shixin
TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTOR GENE CCR3 AND
ANTAGONISTS THEREOF
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive

CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/283,028
FILING DATE: 28-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/720,565
FILING DATE: 30-SEP-1996
APPLICATION NUMBER: PCT/US96/00608
FILING DATE: 19-JAN-1996
APPLICATION NUMBER: US 08/375,199
FILING DATE: 19-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS94-05A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1193 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 92..1156
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-283-028-3

Query Match 68.6%; Score 35; DB 15; Length 1193;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 TTGTGCTTATCCGGGCAAGAACTTATCGAAATACA 51
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Db 1 TTGTGCTTATCCGGGCAAGAACTTATCGAAATACA 35

RESULT 5
US-10-085-783A-39054/c
Sequence 39054, Application US/10085783A
Publication No. US20040037841A1
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2002
CURRENT APPLICATION NUMBER: US/10/085,783A
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 39054
LENGTH: 394
TYPE: DNA
ORGANISM: Human
FEATURE:

NAME/KEY: misc_feature
LOCATION: (67)..(67)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (109)..(109)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (145)..(145)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
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FEATURE:
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NAME/KEY: misc_feature
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LOCATION: (204)..(204)
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NAME/KEY: misc_feature
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FEATURE:
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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OTHER INFORMATION: n is a, c, g, or t

US-10-085-783A-39054
Query Match 51.0%; Score 26; DB 13; Length 394;
Best Local Similarity 72.7%; Pred. No. 0.86;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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Db 366 TANCACAGATTACTTGTTCTTACCCCAAGTAAGATTATAGAA 323
RESULT 6
US-10-242-535A-39054/c
; Sequence 39054, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US 10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39054
; LENGTH: 394.
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (67)..(67)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (109)..(109)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (145)..(145)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (168)..(168)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (187)..(187)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (193)..(193)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (204)..(204)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (224)..(224)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (269)..(269)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (277)..(277)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (287)..(287)

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; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (306)..(306)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (314)..(314)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (348)..(348)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (364)..(364)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (370)..(370)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (393)..(393)
; OTHER INFORMATION: n is a, c, g, or t
;
US-10-242-535A-39054

```

```

Query Match 51.0%; Score 26; DB 16; Length 394;
Best Local Similarity 72.7%; Pred. No. 0.86;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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```

Qy 3 TACCACGTGCTTCTTGTCTTATCCGGCGCAAGACTTATCGAA 46
Db 366 TACACAGATTACTTGTCTTCTTATCCGGCGCAAGACTTATCGAA 323

```

RESULT 7

```

US-10-085-783A-38805/c
; Sequence 38805, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liaw, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38805
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (67)..(67)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (109)..(109)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (145)..(145)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature

```

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; LOCATION: (168)..(168)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (187)..(187)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (193)..(193)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (204)..(204)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (224)..(224)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (269)..(269)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (277)..(277)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (287)..(287)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (314)..(314)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (348)..(348)
; OTHER INFORMATION: n is a, c, g, or t
;
US-10-085-783A-38805

```

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Query Match 49.0%; Score 25; DB 13; Length 396;
Best Local Similarity 70.5%; Pred. No. 2.3;
Matches 31; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

```

```

Qy 3 TACCACGTGCTTCTTGTCTTATCCGGCGCAAGACTTATCGAA 46
Db 366 TACACAGATTACTTGTCTTCTTATCCGGCGCAAGACTTATCGAA 323

```

RESULT 8

```

US-10-242-535A-38805/c
; Sequence 38805, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liaw, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38805
; LENGTH: 396
; TYPE: DNA

```

```

; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 201530
; LENGTH: 669
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-201530

Query Match 47.8%; Score 24.4; DB 13; Length 669;
Best Local Similarity 73.8%; Pred. No. 4.9;
Matches 31; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1 GGTACCACTGGCTTCTTGCTTATCCGGGCAAGACTTAT 42
Db 284 GATAAGCCTGGCTTTTGTGCTTCTCGGGCAATAATGTGT 243

RESULT 10
US-10-027-632-201530/c
; Sequence 201530, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 201530
; LENGTH: 669
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-201530

Query Match 47.8%; Score 24.4; DB 16; Length 669;
Best Local Similarity 73.8%; Pred. No. 4.9;
Matches 31; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1 GGTACCACTGGCTTCTTGCTTATCCGGGCAAGACTTAT 42
Db 284 GATAAGCCTGGCTTTTGTGCTTCTCGGGCAATAATGTGT 243

```

```
RESULT 11
US-10-027-632-201531/c
; Sequence 201531, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 201531
; LENGTH: 1312
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(1312)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-201531
```

```
Query Match 47.8%; Score 24.4; DB 13; Length 1312;
Best Local Similarity 73.8%; Pred.No. 5.9;
Matches 31; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
```

```
Qy 1 GGTACCACTGGTCTTCTGTGCTTATCCGGGCAAGAACTTAT 42
| | | | | | | | | | | | | | | | | | | | | |
Db 284 GATAAGCCTGGTCTTCTGTGCTTCTCGGGCAATAATGTGT 243
```

```
RESULT 12
US-10-027-632-201531/c
; Sequence 201531, Application US/10027632
; Publication No. US200204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
```

```
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 201531
; LENGTH: 1312
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(1312)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-201531
```

```
Query Match 47.8%; Score 24.4; DB 16; Length 1312;
Best Local Similarity 73.8%; Pred.No. 5.9;
Matches 31; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
```

```
Qy 1 GGTACCACTGGTCTTCTGTGCTTATCCGGGCAAGAACTTAT 42
| | | | | | | | | | | | | | | | | | | | | |
Db 284 GATAAGCCTGGTCTTCTGTGCTTCTCGGGCAATAATGTGT 243
```

```
RESULT 13
US-10-027-632-214974
; Sequence 214974, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 214974
; LENGTH: 611
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(611)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-214974
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Query Match 45.9%; Score 23.4; DB 13; Length 611;
Best Local Similarity 67.3%; Pred.No. 13;
Matches 33; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
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Qy 3 TACCACCTGGTCTTCTGTGCTTATCCGGGCAAGAACTTATCGAATACA 51
| | | | | | | | | | | | | | | | | | | | | |
Db 199 TATCAATGGGCTTTTCTGTGCTTATCGAATACA 247
```

```
RESULT 14
US-10-027-632-214974
; Sequence 214974, Application US/10027632
; Publication No. US200204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
```

Db 512 TACCACTCCGCTTATATGCTTCCCGGGTGACTGCTTCTCCTAATACA 560

Search completed: August 2, 2004, 18:14:49
Job time : 250 secs

Qy

3 TACCACCTGGTCTTCCTTGCTTTATCCGGGCAAGAACTTATCGAAATACA 51
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Dβ

199 TATCAATGGGCTTTTTCTGTGTGGCTGCACACTGCATTATGGAAAATAA 247
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```
Query Match      45.9%; Score 23.4; DB 17; Length 1327;
Best Local Similarity 67.3%; Pred. No. 16;
Matches 33; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
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3 TACCACTGGTCTTCTGTGCTTATCCGGGCAAGAACTTATCGAAATACA 51

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 16:05:29 ; Search time 47 Seconds
(without alignments)
602.181 Million cell updates/sec

Title: US-10-068-067-16

Perfect score: 51
Sequence: I ggtaccactggtcttctgt.....caagaacttcgaataaca 51

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*

5: /cgn2_6/ptodata/2/ina/PTCUTS_COMB.seq.*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	35	68.6	1193	US-08-720-565-3	Sequence 3, Appli
2	22	43.1	1341	US-09-543-681A-1577	Sequence 1577, Ap
3	21.4	42.0	912	US-09-420-786A-4	Sequence 4, Appli
C 4	21	41.2	2521	US-09-620-312D-777	Sequence 777, App
C 5	21	41.2	4021	US-09-453-702B-197	Sequence 197, App
C 6	20.8	40.8	987	US-09-599-360B-58	Sequence 58, Appl
C 7	20.8	40.8	13440	US-08-961-527-128	Sequence 128, App
C 8	20.6	40.4	2553	US-09-328-352-2457	Sequence 2457, Ap
C 9	20.4	40.0	1000	US-09-280-116-134	Sequence 134, App
C 10	20.2	39.6	1023	US-08-785-065-2	Sequence 2, Appli
C 11	20.2	39.6	1023	US-09-151-412-2	Sequence 5, Appli
C 12	20.2	39.6	4775	US-09-220-132-5	Sequence 52, Appl
C 13	20	39.2	675	US-08-821-994-52	Sequence 53, Appl
C 14	20	39.2	690	US-08-821-994-53	Sequence 14, Appl
C 15	20	39.2	897	US-08-899-330-14	Sequence 19, Appl
C 16	20	39.2	1026	US-09-655-908-19	Sequence 86, Appl
C 17	20	39.2	1102	US-08-821-994-86	Sequence 62, Appl
C 18	20	39.2	1434	US-08-821-994-62	Sequence 6787, Ap
C 19	19.8	38.8	1119	US-09-489-039A-6787	Sequence 3259, Ap
C 20	19.8	38.8	1131	US-09-107-532A-3259	Sequence 3259, Ap
C 21	19.8	38.8	1231	US-09-454-279-13	Sequence 13, Appl
C 22	19.8	38.8	1827	US-09-543-681A-3546	Sequence 3546, Ap
C 23	19.8	38.8	1827	US-08-448-194-5	Sequence 5, Appli
C 24	19.8	38.8	2809	US-08-867-921-5	Sequence 5, Appli
C 25	19.8	38.8	3114	US-09-543-681A-3505	Sequence 1, Appli
C 26	19.8	38.8	3286	US-08-363-124A-1	Sequence 168, App
C 27	19.6	38.4	500	US-09-669-751-168	

ALIGNMENTS

RESULT 1

US-08-720-565-3

; Sequence 3, Application US/08720565

; Patent No. 6537764

; GENERAL INFORMATION:

; APPLICANT: Gerard, Craig J.

; APPLICANT: Gerard, No. 6537764ma P.

; APPLICANT: Mackay, Charles R.

; APPLICANT: Ponath, Paul D.

; APPLICANT: Post, Theodore W.

; APPLICANT: Qin, Shixin

; TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTOR GENE CCR3 AND

; TITLE OF INVENTION: ANTAGONISTS THEREOF

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

; STREET: Two Militia Drive

; CITY: Lexington

; STATE: MA

; COUNTRY: USA

; ZIP: 02173

; COMPUTER TYPE: Floppy disk

; MEDIUM TYPE: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/720,565

; FILING DATE: 30-SEP-1996

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US96/00608

; FILING DATE: 19-JAN-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/375,199

; FILING DATE: 19-JAN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Brook, David E.

; REGISTRATION NUMBER: 22,592

; REFERENCE/DOCKET NUMBER: LKS94-05A2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-861-6240

; TELEFAX: 617-861-9540

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1193 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cdna

Sequence 3245, Ap
Sequence 7, Appli
Sequence 7, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 3259, Ap
Sequence 4, Appli
Sequence 98, Appli
Sequence 1, Appli
Sequence 1178, Ap
Sequence 1, Appli
Sequence 1, Appli
Sequence 5353, Ap
Sequence 2698, Ap
Sequence 131, App
Sequence 3341, App
Sequence 278, App
Sequence 5890, Ap

28 19.6 38.4 597 4 US-09-621-976-3245
29 19.6 38.4 982 4 US-09-221-017B-7
30 19.6 38.4 28720 4 US-09-341-587-7
31 19.6 38.4 84495 4 US-09-797-906-3
32 19.6 38.4 1664976 4 US-08-916-421B-1
33 19.4 38.0 268 4 US-09-313-294A-3259
34 19.4 38.0 549 1 US-08-367-198A-4
35 19.4 38.0 655 4 US-09-023-655-98
36 19.4 38.0 970 1 US-08-367-198A-1
37 19.4 38.0 1257 4 US-09-328-352-1178
38 19.4 38.0 129908 4 US-09-585-858-1
39 19.4 38.0 1230025 4 US-09-198-452A-1
40 19.2 37.6 339 4 US-09-489-039A-5353
41 19.2 37.6 461 4 US-09-621-976-2698
42 19.2 37.6 483 4 US-09-328-352-131
43 19.2 37.6 505 4 US-09-621-976-3341
44 19.2 37.6 580 4 US-09-221-017B-278
45 19.2 37.6 1413 4 US-09-489-039A-5890

APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

;; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
;; FILE REFERENCE: GTC99-03PA
;; CURRENT APPLICATION NUMBER: US/09/328,352
;; CURRENT FILING DATE: 1999-06-04
;; NUMBER OF SEQ ID NOS: 8252
;; SEQ ID NO 2457
;; LENGTH: 2553
;; TYPE: DNA
;; ORGANISM: Acinetobacter baumannii
US-09-328-352-2457

Query Match 40.4%; Score 20.6; DB 4; Length 2553;
Best Local Similarity 62.7%; Pred. No. 28;
Matches 32; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 1 GGTACCACTGGTCTTCTGTGCTTATCCGGCGCAAGAACTTATCGAAATACA 51
|||||
Db 336 GGTAAACAGGCTTTGCATTCATTCGACGAGTACTTTTAAACAAA 286

RESULT 9

US-09-280-116-134
; Sequence 134, Application US/09280116A
; Patent No. 631427
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
; FILE REFERENCE: 5800-24, 035800/176965
; CURRENT APPLICATION NUMBER: US/09/280,116A
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 134
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: trypsin-like serine proteases
; NAME/KEY: misc feature
; LOCATION: (1)..(1000)
; OTHER INFORMATION: n = a, t, c or g
US-09-280-116-134

Query Match 40.0%; Score 20.4; DB 4; Length 1000;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 4 ACCACTGGTCTTCTGTGCTTATCCGGGCA 33
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Db 223 ACCATTGGTCTTCTGTGCTTATTCGGCA 252

RESULT 10

US-08-785-065-2/c
; Sequence 2, Application US/08785065
; Patent No. 5814451
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL SUBUNITS OF NADH DEHYDROGENASE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSEQ for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/785,065
;; FILING DATE: Herewith
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:

;; ATTORNEY/AGENT INFORMATION:
;; NAME: Billings, Lucy J.
;; REGISTRATION NUMBER: 36,749
;; REFERENCE/DOCKET NUMBER: PF-0187 US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-855-0555
;; TELEFAX: 415-845-4166
;; TELEX:

;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1023 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; LIBRARY: Consensus
;; CLONE: Consensus
US-08-785-065-2

Query Match 39.6%; Score 20.2; DB 1; Length 1023;
Best Local Similarity 63.3%; Pred. No. 30;
Matches 31; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 2 GTACCACTGGTCTTCTGTGCTTATCCGGCGCAAGAACTTATCGAAATAC 50
|||||
Db 383 GGACACCTGAACCTGTGGACATACCTTGGGCAAGATTTCAGCCACATAC 335

RESULT 11

US-09-151-412-2/c
; Sequence 2, Application US/09151412
; Patent No. 6399345
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL SUBUNITS OF NADH DEHYDROGENASE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA: US/09/151,412
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/785,065
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0187 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166

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;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1023 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; IMMEDIATE SOURCE:
;   LIBRARY: Consensus
;   CLONE: Consensus
US-09-151-412-2

Query Match      39.6%; Score 20.2; DB 4; Length 1023;
Best Local Similarity 63.3%; Pred. No. 30;
Matches 31; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 2 GTACCACTGCTCTTCTGCTTATCCGGGCAAGAACTTATCGAAATAC 50
Db 383 GGACACCTGAACCTTGTGGACATACCTTGGGCAAGATTTTCAGCCACATAC 335

RESULT 12
US-09-220-132-5
; Sequence 5, Application US/09220132
; Patent No. 6506607
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT
;   OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 07334-074001
; CURRENT APPLICATION NUMBER: US/09/220,132
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 60/079,303
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: US 60/068,821
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4775
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-220-132-5

Query Match      39.6%; Score 20.2; DB 4; Length 4775;
Best Local Similarity 75.8%; Pred. No. 52;
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 8 CTGCTCTTCTTGTGCTTATCCGGGCAAGAACTT 40
Db 2647 CTAGCTTCTTGTTCATATAGGGGCAAAATTT 2679

RESULT 13
US-08-821-994-52
; Sequence 52, Application US/08821994A
; Patent No. 6228643
; GENERAL INFORMATION:
; APPLICANT: Greenland, Andrew J
; APPLICANT: Thomas, Didier RP
; APPLICANT: Jepson, Ian
; TITLE OF INVENTION: Promoters
; FILE REFERENCE: PPD 50108
; CURRENT APPLICATION NUMBER: US/08/821,994A
; CURRENT FILING DATE: 1997-03-22
; EARLIER APPLICATION NUMBER: PCT/GB97/00729
; EARLIER FILING DATE: 1997-03-18
; EARLIER APPLICATION NUMBER: GB 9606062.9
; EARLIER FILING DATE: 1996-03-22
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 675
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;
; TYPE: DNA
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 388, 390, 391, 402, 403, 439..441
; OTHER INFORMATION: n is unknown
US-08-821-994-52

Query Match      39.2%; Score 20; DB 3; Length 675;
Best Local Similarity 65.9%; Pred. No. 32;
Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 2 GTACCACTGCTCTTCTTGTGCTTATCCGGGCAAGAACTTATCGA 45
Db 568 GTAACAGGAGAACTCGTATCTTTGTCCGAACAAGAACTTGTGCGA 611

RESULT 14
US-08-821-994-53
; Sequence 53, Application US/08821994A
; Patent No. 6228643
; GENERAL INFORMATION:
; APPLICANT: Greenland, Andrew J
; APPLICANT: Thomas, Didier RP
; APPLICANT: Jepson, Ian
; TITLE OF INVENTION: Promoters
; FILE REFERENCE: PPD 50108
; CURRENT APPLICATION NUMBER: US/08/821,994A
; CURRENT FILING DATE: 1997-03-22
; EARLIER APPLICATION NUMBER: PCT/GB97/00729
; EARLIER FILING DATE: 1997-03-18
; EARLIER APPLICATION NUMBER: GB 9606062.9
; EARLIER FILING DATE: 1996-03-22
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 690
; TYPE: DNA
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 403, 406, 417..419, 455, 456
; OTHER INFORMATION: n is unknown
US-08-821-994-53

Query Match      39.2%; Score 20; DB 3; Length 690;
Best Local Similarity 65.9%; Pred. No. 32;
Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 2 GTACCACTGCTCTTCTTGTGCTTATCCGGGCAAGAACTTATCGA 45
Db 583 GTAACAGGAGAACTCGTATCTTTGTCCGAACAAGAACTTGTGCGA 626

RESULT 15
US-08-899-330-14/c
; Sequence 14, Application US/08899330
; Patent No. 617275
; GENERAL INFORMATION:
; APPLICANT: CORUZZI, GLORIA
; APPLICANT: LAM, HON-MING
; APPLICANT: HSIEH, MING-HSIUN
; TITLE OF INVENTION: PLANT NITROGEN REGULATORY
;   P-II GENES
; TITLE OF INVENTION: P-II GENES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,330
; FILING DATE: 23-JUL-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/022,328
; FILING DATE: 24-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 5914-042-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)7909090
; TELEFAX: (212)8699741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 897 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; US-08-899-330-14

Query Match      39.2%; Score 20; DB 3; Length 897;
Best Local Similarity 65.9%; Pred. No. 35;
Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy      7  ACTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGAAATAC 50
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Db     861  ACTCCTCTTCTGTATTATCTTGCAAGCACTTGACAAATC 818

Search completed: August 2, 2004, 16:56:31
Job time : 51 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 16:14:47 ; Search time 1821 Seconds
(without alignments)
836.338 Million cell updates/sec

Title: US-10-068-067-16

Perfect score: 51

Sequence: 1 ggtaccactggtctcttgt.....caagaacttatcgaaataca 51

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:

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1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution..

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	70.6	876	12	BI906283
2	25.8	50.6	1006	10	BF568349
C 3	24.6	48.2	461	9	AV947614
C 4	24.6	48.2	556	9	AV977709

C 5	24.6	48.2	657	9	AV672256
C 6	24.6	48.2	671	13	BW315750
C 7	24.6	48.2	673	29	AG131818
C 8	24.6	48.2	689	13	BW238153
C 9	24.6	48.2	699	9	AV675510
C 10	24.6	48.2	747	28	AZ516237
C 11	24.4	47.8	516	13	BQ988753
C 12	24.4	47.8	639	13	BQ855999
C 13	24.4	47.8	636	13	BQ990860
C 14	24.4	47.8	701	13	BQ855345
C 15	24.4	47.8	711	13	BQ857473
C 16	24.4	47.8	713	13	BQ993947
C 17	24.4	47.8	740	13	BQ847844
C 18	24.4	47.8	741	13	BQ986512
C 19	24.4	47.8	754	13	BQ986671
C 20	24	47.1	238	10	BB646936
C 21	24	47.1	521	13	CA026489
C 22	24	47.1	537	28	BH775634
C 23	24	47.1	545	14	CF370689
C 24	24	47.1	563	14	CF370660
C 25	24	47.1	572	14	CD909873
C 26	24	47.1	574	13	BQ240272
C 27	24	47.1	603	10	BE405787
C 28	24	47.1	607	14	CA732078
C 29	24	47.1	611	14	CA600664
C 30	24	47.1	624	13	BQ465033
C 31	24	47.1	645	13	BQ805758
C 32	24	47.1	667	9	AI725089
C 33	24	47.1	668	13	BQ295372
C 34	24	47.1	689	13	CA013250
C 35	24	47.1	753	14	CD921720
C 36	24	47.1	762	14	CF132850
C 37	24	47.1	887	12	BM816941
C 38	24	47.1	943	12	BI224795
C 39	23.8	46.7	576	28	BH354963
C 40	23.8	46.7	722	12	BM292491
C 41	23.8	46.7	942	28	CC438714
C 42	23.8	46.7	1057	28	CC258247
C 43	23.6	46.3	208	9	AI509242
C 44	23.6	46.3	282	29	CC791444
C 45	23.6	46.3	316	14	CB708794

ALIGNMENTS

BI906283 876 bp mRNA linear EST 16-OCT-2001
LOCUS 603083222F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5212541 5',
DEFINITION mRNA sequence.
ACCESSION BI906283
VERSION BI906283.1 GI:16168946
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 876)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11533 row: k column: 06
High quality sequence stop: 800.

FEATURES
source

Location/Qualifiers
1. .876
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5212541"
/tissue_type="leukocyte"
/lab_host="DH108"
/clone_lib="NIH_MGC 118"
/notes="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 70.8%; Score 36; DB 12; Length 876;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CTTGTGCTTATCCGGGCAAGAACTTATCGAATACA 51
Db 1 CTTGTGCTTATCCGGGCAAGAACTTATCGAATACA 36

RESULT 2

BF568349 1006 bp mRNA linear EST 12-DEC-2000
LOCUS 602184537F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300521 5',
DEFINITION RNA sequence.

ACCESSION BF568349
VERSION BF568349.1 GI:11641729
KEYWORDS EST.

SOURCE
ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1006)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov

Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LCM159 row: j column: 10
High quality sequence stop: 739.

FEATURES
source

Location/Qualifiers
1. .1006
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4300521"
/tissue_type="epithelioid carcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC 42"
/notes="Organ: pancreas; Vector: pOTEB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).

ORIGIN Note: this is a NIH_MGC Library. |"

Query Match 50.6%; Score 25.8; DB 10; Length 1006;
Best Local Similarity 81.1%; Pred. No. 20;
Matches 30; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4 ACCACTGCTCTCTTGTGCTTATCCGGGCAAGAACTT 40
Db 705 AACAACTGCTCTCTTGTGCTTATCTGACCATGAATT 741

RESULT 3

AV947614/c

LOCUS AV947614 Nori Satoh unpublished cDNA library, young adult Ciona
DEFINITION intestinalis cDNA clone ciad01f07 5', mRNA sequence.

ACCESSION AV947614

VERSION AV947614.1 GI:19425373

KEYWORDS

SOURCE

ORGANISM Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.

REFERENCE 1 (bases 1 to 461)

AUTHORS Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.

TITLE Expressed genes in Ciona intestinalis

JOURNAL

COMMENT Unpublished (2000)

Contact: Nori Satoh

Department of Zoology

Kyoto University

Sakyo-ku, Kyoto, Kyoto 606-8502, Japan

Tel: 81-75-753-4081

Fax: 81-75-705-1113

Email: satoh@ascidian.zool.kyoto-u.ac.jp.

FEATURES

source

1. .461
Location/Qualifiers

/organism="Ciona intestinalis"

/mol_type="mRNA"

/db_xref="taxon:7719"

/clone="ciad01f07"

/tissue_type="whole animal"

/dev_stage="young adult"

/clone_lib="Nori Satoh unpublished cDNA library, young adult"

ORIGIN

Query Match 48.2%; Score 24.6; DB 9; Length 461;

Best Local Similarity 70.2%; Pred. No. 51;

Matches 33; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 GGTACCACTGCTCTTGTGCTTATCCGGGCAAGAACTTATCGAAA 47

Db 421 GGTGCCCGCGGCTCTTGTGCTTATCCGGGCAAGAACTTATCGAAA 375

RESULT 4

AV977709/c

LOCUS AV977709 Nori Satoh unpublished cDNA library, egg Ciona

DEFINITION intestinalis cDNA clone cie46b20 5', mRNA sequence.

ACCESSION AV977709

VERSION AV977709.1 GI:19467475

KEYWORDS

SOURCE

ORGANISM

Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.

REFERENCE 1 (bases 1 to 556)

AUTHORS Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.

TITLE Expressed genes in Ciona intestinalis

JOURNAL

COMMENT Unpublished (2000)

Contact: Nori Satoh

```

Department of Zoology
Kyoto University
Sakyo-Ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satho@ascidian.zool.kyoto-u.ac.jp.

FEATURES
source
    /organism="Ciona intestinalis"
    /mol_type="mRNA"
    /db_xref="taxon:7719"
    /clone="cig46b20"
    /tissue_type="whole animal"
    /dev_stage="egg"
    /clone_lib="Nori Satoh unpublished cDNA library, egg"

ORIGIN
Query Match      48.2%; Score 24.6; DB 9; Length 556;
Best Local Similarity 70.2%; Pred. No. 53;
Matches 33; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY   1  GTTACACTGGCTTCCTGTTATCCGGCAAGAACTTATCGAAA 47
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Db   336  GGTCGCCGGGCTTCTTGTCATCTTTGGGCAATGCTACCGGAA 290

RESULT 5
AV672256/c
LOCUS          AV672256        657 bp mRNA linear EST 05-OCT-2000
DEFINITION     AV672256 Nori Satoh unpublished cDNA library Ciona intestinalis
                cDNA clone citb3cs 5', mRNA sequence.
ACCESSION      AV672256
VERSION        AV672256.1 GI:10110255
KEYWORDS       EST.
SOURCE         Ciona intestinalis
ORGANISM       Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
                Phlebobranchia; Cionidae; Ciona.
REFERENCE      1 (bases 1 to 657)
AUTHORS        Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
TITLE          Expressed genes in Ciona intestinalis
JOURNAL        Unpublished (2000)
COMMENT        Contact: Nori Satoh
                Department of Zoology
                Kyoto University
                Sakyo-Ku, Kyoto, Kyoto 606-8502, Japan
                Tel: 81-75-753-4081
                Fax: 81-75-705-1113
                Email: satho@ascidian.zool.kyoto-u.ac.jp.

FEATURES
source
    /organism="Ciona intestinalis"
    /mol_type="mRNA"
    /db_xref="taxon:7719"
    /clone="citb3cs"
    /tissue_type="whole animal"
    /dev_stage="tailbud"
    /clone_lib="Nori Satoh unpublished cDNA library"

ORIGIN
Query Match      48.2%; Score 24.6; DB 9; Length 657;
Best Local Similarity 70.2%; Pred. No. 55;
Matches 33; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY   1  GTTACACTGGCTTCCTGTTATCCGGCAAGAACTTATCGAAA 47
     |||||
Db   310  GGTCGCCGGGCTTCTTGTCATCTTTGGGCAATGCTACCGGAA 264

RESULT 6
EW315750/c
LOCUS          EW315750        671 bp mRNA linear EST 11-NOV-2002
DEFINITION     BW315750 Nori Satoh unpublished cDNA library, heart Ciona
                intestinalis
                cDNA clone ciht029m20 5', mRNA sequence.
ACCESSION      BW315750
VERSION        BW315750.1 GI:24896434
KEYWORDS       EST.
SOURCE         Ciona intestinalis
ORGANISM       Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
                Phlebobranchia; Cionidae; Ciona.
REFERENCE      1 (bases 1 to 671)
AUTHORS        Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
TITLE          Expressed genes in Ciona intestinalis (2002c)
JOURNAL        Unpublished (2002)
COMMENT        Contact: Nori Satoh
                Department of Zoology
                Kyoto University
                Sakyo-Ku, Kyoto, Kyoto 606-8502, Japan
                Tel: 81-75-753-4081
                Fax: 81-75-705-1113
                Email: satho@ascidian.zool.kyoto-u.ac.jp.

FEATURES
source
    /organism="Ciona intestinalis"
    /mol_type="mRNA"
    /db_xref="taxon:7719"
    /clone="ciht029m20"
    /tissue_type="heart"
    /clone_lib="Nori Satoh unpublished cDNA library, heart"

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Query Match      48.2%; Score 24.6; DB 13; Length 671;
Best Local Similarity 70.2%; Pred. No. 55;
Matches 33; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY   1  GGTACCACCTGGCTTCCTGTTATCCGGCAAGAACTTATCGAAA 47
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Db   523  GGTCGCCGGGCTTCTTGTCATCTTTGGGCAATGCTACCGGAA 477

RESULT 7
AG131818
LOCUS          AG131818        673 bp DNA linear GSS 04-NOV-2001
DEFINITION     Pan troglodytes DNA, clone: PTB-144A01.R, genomic survey sequence.
ACCESSION      AG131818
VERSION        AG131818.1 GI:16661496
KEYWORDS       GSS.
SOURCE         Pan troglodytes (chimpanzee)
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE      1
AUTHORS        Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
                Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE          BAC end sequences of Library PTB
JOURNAL        Unpublished
REFERENCE      2 (bases 1 to 673)
AUTHORS        Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
                Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE          Direct Submission
JOURNAL        Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
                and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
                1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                (E-mail:chimbes@gsc.riken.go.jp, URL:http://hgpc.gsc.riken.go.jp/,
                Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT        Clones are derived from the chimpanzee BAC library PTB This BAC end
                was generated during the R&D process and may have higher chance of
                clone tracking errors.
                PRIMERS
                Sequencing: M13Rev
                LIBRARY
                Vector : pKS145
                R.Site 1 : SacI
                R.Site 2 : SacI.
                Location/Qualifiers

FEATURES

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source
1. .673
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-144A01.R"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

ORIGIN
Query Match 48.2%; Score 24.6; DB 29; Length 673;
Best Local Similarity 70.2%; Pred. No. 55;
Matches 33; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 4 ACCACTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGAAATAC 50
Db 126 ACATCTGCTCTCTTGCTTATCCAGCGGAGAGGTGATATCAATAC 172

RESULT 8
BW238153/c
LOCUS
DEFINITION BW238153 Nori Satoh unpublished cDNA library, tailbud embryo Ciona
intestinalis cDNA clone citb058p22 5', mRNA sequence.
ACCESSION BW238153.1 GI:24760342
VERSION
KEYWORDS
SOURCE
ORGANISM
Ciona intestinalis
Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Clonidae; Ciona.
REFERENCE
1 (bases 1 to 689)
Satou, Y., Shin-i, T., Kohara, Y. and Satoh, N.
Expressed genes in Ciona intestinalis (2002c)
Unpublished (2002)
JOURNAL
COMMENT
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.

FEATURES
Location/Qualifiers
1. .689
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="citb058p22"
/tissue_type="whole animal"
/dev_stage="tailbud embryo"
/clone_lib="Nori Satoh unpublished cDNA library, tailbud
embryo"

ORIGIN
Query Match 48.2%; Score 24.6; DB 13; Length 689;
Best Local Similarity 70.2%; Pred. No. 56;
Matches 33; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 GGTACCACTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGAAA 47
Db 294 GGTGCCCGGGTCTTCTTGCTATCTTTGGGCAATGCTACCGGAA 248

RESULT 9
AV675510/c
LOCUS
DEFINITION AV675510 Nori Satoh unpublished cDNA library Ciona intestinalis
cDNA clone citb12k10 5', mRNA sequence.
ACCESSION AV675510
VERSION
KEYWORDS
SOURCE
ORGANISM
Ciona intestinalis
Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Clonidae; Ciona.
REFERENCE
1 (bases 1 to 699)
Satou, Y., Shin-i, T., Kohara, Y. and Satoh, N.
Expressed genes in Ciona intestinalis (2002c)
Unpublished (2002)
JOURNAL
COMMENT
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.

FEATURES
Location/Qualifiers
1. .699
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="citb058p22"
/tissue_type="whole animal"
/dev_stage="tailbud embryo"
/clone_lib="Nori Satoh unpublished cDNA library, tailbud
embryo"

ORIGIN
Query Match 48.2%; Score 24.6; DB 29; Length 673;
Best Local Similarity 70.2%; Pred. No. 55;
Matches 33; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 4 ACCACTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGAAATAC 50
Db 126 ACATCTGCTCTCTTGCTTATCCAGCGGAGAGGTGATATCAATAC 172

RESULT 8
BW238153/c
LOCUS
DEFINITION BW238153 Nori Satoh unpublished cDNA library, tailbud embryo Ciona
intestinalis cDNA clone citb058p22 5', mRNA sequence.
ACCESSION BW238153.1 GI:24760342
VERSION
KEYWORDS
SOURCE
ORGANISM
Ciona intestinalis
Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Clonidae; Ciona.
REFERENCE
1 (bases 1 to 689)
Satou, Y., Shin-i, T., Kohara, Y. and Satoh, N.
Expressed genes in Ciona intestinalis (2002c)
Unpublished (2002)
JOURNAL
COMMENT
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.

FEATURES
Location/Qualifiers
1. .689
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="citb058p22"
/tissue_type="whole animal"
/dev_stage="tailbud embryo"
/clone_lib="Nori Satoh unpublished cDNA library, tailbud
embryo"

ORIGIN
Query Match 48.2%; Score 24.6; DB 13; Length 689;
Best Local Similarity 70.2%; Pred. No. 56;
Matches 33; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 GGTACCACTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGAAA 47
Db 294 GGTGCCCGGGTCTTCTTGCTATCTTTGGGCAATGCTACCGGAA 248

RESULT 9
AV675510/c
LOCUS
DEFINITION AV675510 Nori Satoh unpublished cDNA library Ciona intestinalis
cDNA clone citb12k10 5', mRNA sequence.
ACCESSION AV675510
VERSION
KEYWORDS
SOURCE
ORGANISM
Ciona intestinalis
Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Clonidae; Ciona.
REFERENCE
1 (bases 1 to 699)
Satou, Y., Shin-i, T., Kohara, Y. and Satoh, N.
Expressed genes in Ciona intestinalis (2002c)
Unpublished (2002)
JOURNAL
COMMENT
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.

FEATURES
Location/Qualifiers
1. .699
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="citb12k10"
/tissue_type="whole animal"
/dev_stage="tailbud"
/clone_lib="Nori Satoh unpublished cDNA library"

ORIGIN
Query Match 48.2%; Score 24.6; DB 9; Length 699;
Best Local Similarity 70.2%; Pred. No. 56;
Matches 33; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 GGTACCACTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGAAA 47
Db 391 GGTGCCCGGGTCTTCTTGCTATCTTTGGGCAATGCTACCGGAA 345

RESULT 10
AZ516237
LOCUS
DEFINITION RPCI-11-269M6.TJB RPCI-11 Homo sapiens genomic clone RPCI-11-269M6,
genomic survey sequence.
ACCESSION AZ516237
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 747)
Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and
Venter, J.C.
BAC end sequences of library RPCI-11
Unpublished (1997)
Other GSSs: RPCI-11-269M6.TV
JOURNAL
COMMENT
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (inico@resgen.com). BAC end search page:
http://www.tigr.org/tcdb/humgen/bac_end_search/bac_end_search.html.
This BAC end was generated during the R&D process and may have
higher chance of clone tracking errors.
Seg primer: SP6
Class: BAC ends.
Location/Qualifiers
1. .747
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:7603205"

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/db_xref="taxon:9606"
/clone="RPC1-11-269M6"
/sex="Male"
/cell_type="Lymphocytes"
/clone_lib="RPC1-11"
/notes="vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI;
RPC111 Human Male BAC Library"

ORIGIN

Query Match      48.2%; Score 24.6; DB 28; Length 747;
Best Local Similarity 70.2%; Pred. No. 56;
Matches 33; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 4 ACCACTGCTCTTCTGTCTATCCGGGCAAGAACTTATCGAATAC 50
    |||||
Db 628 ACATCTGCTCTCTTGTCTCTAGCAGGCGGAGAGGTGATGTCATAC 674

RESULT 11
BQ988753
LOCUS      BQ988753
DEFINITION BQ988753 516 bp mRNA linear EST 21-AUG-2002
ACCESSION QG215M08.yg.ab1 QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
VERSION    QG215M08 mRNA sequence.
KEYWORDS   EST.
SOURCE     Lactuca sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
Cichorieae; Lactuca.
REFERENCE  1 (bases 1 to 516)
AUTHORS   Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J.,
Ellison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y.,
Lai,Z., Church,S., Jackson,L. and Bradford,K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://comgenomics.ucdavis.edu/
JOURNAL   Unpublished (2002)
COMMENT    Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QG_CA_Contig4248, see http://cgdb.ucdavis.edu/
for details.
Plate: QG15 row: M column: 08.

FEATURES             source
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    /db_xref="taxon:4236"
    /clone="QG215M08"
    /lab_host="E.coli"
    /clone_lib="QG_EFGHJ lettuce serriola"
    /note="Vector: pBRCNASfiAB; The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgdb.ucdavis.edu/
TAG LIB=QG_EFGHJ lettuce serriola
TAG_SEQ=TGCCATCGG3"

ORIGIN

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Query Match      47.8%; Score 24.4; DB 13; Length 516;
Best Local Similarity 73.8%; Pred. No. 63;
Matches 31; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 4 ACCACTGCTCTTCTGTCTATCCGGGCAAGAACTTATCGA 45
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Db 104 ACAAAGAGGTTAGTGTCTGTTATCTGAGCAAGAACTTATCGA 145

RESULT 12
BQ855999
LOCUS      BQ855999
DEFINITION BQ855999 639 bp mRNA linear EST 14-AUG-2002
ACCESSION QGB28F02.yg.ab1 QG_ABCDI lettuce salinas Lactuca sativa cDNA clone
VERSION    QGB28F02 mRNA sequence.
KEYWORDS   EST.
SOURCE     Lactuca sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
Cichorieae; Lactuca.
REFERENCE  1 (bases 1 to 639)
AUTHORS   Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J.,
Ellison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y.,
Lai,Z., Church,S., Jackson,L. and Bradford,K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://comgenomics.ucdavis.edu/
JOURNAL   Unpublished (2002)
COMMENT    Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QG_CA_Contig4248, see http://cgdb.ucdavis.edu/
for details.
Plate: QGB28 row: F column: 02.

FEATURES             source
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    /lab_host="E.coli"
    /clone_lib="QG_ABCDI lettuce salinas"
    /note="Vector: pBRCNASfiAB; The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgdb.ucdavis.edu/
TAG TISSUE=flowers post-fertilized
TAG LIB=QG_ABCDI lettuce salinas
TAG_SEQ=TGCCATCGG3"

ORIGIN

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Query Match      47.8%; Score 24.4; DB 13; Length 639;
Best Local Similarity 73.8%; Pred. No. 56;
Matches 31; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 4 ACCACTGCTCTTCTGTCTATCCGGGCAAGAACTTATCGA 45
    |||||
Db 171 ACAAAGAGGTTAGTGTCTGTTATCTGAGCAAGAACTTATCGA 212

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TITLE Lai, Z., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
JOURNAL Unpublished (2002)
COMMENT Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]
belongs to contig QG_CA_Contig4248, see http://cgdb.ucdavis.edu/
for details.

Plate: QGB7 row: J column: 21.

FEATURES

Source

1..711

/organism="Lactuca sativa"

/mol_type="mRNA"

/cultivar="Salinas"

/db_xref="taxon:4236"

/clone="QGB7J21"

/lab_host="E.coli"

/clone_lib="QG-ABCDI lettuce salinas"

/note="Vector: pBRCDNASfiAB; The library was constructed

from 10 different sources of RNA from a single genotype.

Separate cDNAs were generated using primers that

incorporated unique 5' and 3' tags to distinguish each

source of RNA. cDNAs were then pooled, size-fractionated,

directionally cloned into a custom medium-copy vector and

transformations made with four size classes to minimize

size bias. Details of each source of RNA and library

construction can be obtained at http://cgdb.ucdavis.edu/

TAG TISSUE=flowers post-fertilized

TAG_LIB=QG-ABCDI lettuce salinas

TAG_SEQ=TCGTCATCGG

ORIGIN

Query Match 47.8%; Score 24.4; DB 13; Length 711;
Best Local Similarity 73.8%; Pred. No. 67;
Matches 31; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 4 ACCACTGCTCTTCTTGTCTTATCGGCGCAAGAACTTATCGA 45

Db 294 AACAAAGGAGTTAGTGTCTTATCTGAGCAAGAACTTATCGA 335

Search completed: August 2, 2004, 17:27:09
Job time : 1829 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 14:48:09 ; Search time 240 Seconds

(without alignments)
902.742 Million cell updates/sec

Title: US-10-068-067-16

Perfect score: 51

Sequence: 1 ggtaccactgtcttcttctgt.....caagaacttatcgaaataca 51

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_29Jan04.*

1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002s.*

7: Geneseqn2003as.*

8: Geneseqn2003bs.*

9: Geneseqn2003cs.*

10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	51	100.0	51	6	ABQ78514 Nucleotid
2	51	100.0	51	6	ABQ78519 Nucleotid
3	51	100.0	2895	6	ABQ78513 Nucleotid
4	35	68.6	1193	2	AAT31335 CC-chemok
5	35	68.6	1193	2	AAV07403 Human C-C
6	22.4	43.9	1342	7	ADA20738 Wheat cDN
7	22.4	43.9	1343	7	ADA20746 Wheat cDN
8	22.2	43.5	420	3	AH30283 Human col
9	22.2	43.5	1313	4	AAf74867 Leishmani
10	22.2	43.5	1719	6	ABK73357 Bacillus
11	22.2	43.5	1861	6	AAS62217 CDNA sequ
12	22.2	43.5	2102	7	AAS26089 Human cDN
13	22.2	43.5	2102	7	ABX73430 Human nov
14	22.2	43.5	2543	4	AAH14667 Human cDN
15	22.2	43.5	2704	4	AAK51701 Human pol
16	22.2	43.5	2784	4	AAS25988 Human cDN
17	22.2	43.5	2784	7	ABX73329 Human nov
18	22.2	43.5	3036	4	AAS2685 Human pol
19	22.2	43.5	3048	4	AAH14479 Human cDN
20	22	43.1	22	6	ABQ78515 Nucleotid
21	22	43.1	22	6	ABQ78516 Nucleotid
22	22	43.1	22	6	ABQ78521 Nucleotid
23	22	43.1	92879	9	ADC85431 Mouse Nr3

c

c	24	22	43.1	92880	8	ADA02951	Ada02951 Mouse Nr3
c	25	22	43.1	92880	9	ADB72689	ADB72689 Mouse Nr3
c	26	21.8	42.7	4305	2	AAx87945	AAx87945 Candida c
c	27	21.8	42.7	4646	8	ADA36974	Ada36974 Prostagla
c	28	21.6	42.4	290	2	AAQ77203	Aaq77203 Human gen
c	29	21.4	42.0	196	2	AAZ14026	Aaz14026 Human gen
c	30	21.4	42.0	466	6	ABL83795	Ab183795 Human ova
c	31	21.4	42.0	582	4	AAI19127	Aai19127 Probe #90
c	32	21.4	42.0	582	4	ABA64130	Abi64130 Human fce
c	33	21.4	42.0	582	4	AAI44275	Aai44275 Probe #12
c	34	21.4	42.0	582	4	ABA31289	Abi31289 Probe #97
c	35	21.4	42.0	582	4	AAK38326	Aak38326 Human bon
c	36	21.4	42.0	582	4	AAK12612	Aak12612 Human bra
c	37	21.4	42.0	582	4	ABS37938	Abi37938 Human liv
c	38	21.4	42.0	582	6	ABS12379	Abi12379 Human liv
c	39	21.4	42.0	745	4	AAS44643	Aas44643 Human ful
c	40	21.4	42.0	912	3	AAAS0335	Aaa90335 Arabidops
c	41	21.4	42.0	1318	3	AAC54012	Aac54012 Arabidops
c	42	21.4	42.0	1323	3	AAC36648	Aac36648 Arabidops
c	43	21.4	42.0	1540	6	ABL88067	Ab188067 Aquifex a
c	44	21.4	42.0	2000	6	ABZ14931	Abz14931 Arabidops
c	45	21.4	42.0	2108	4	AAH15845	Aah15845 Human cDN

ALIGNMENTS

RESULT 1	ABQ78514	ID	ABQ78514 standard; DNA; 51 BP.
XX	AC	ABQ78514;	
XX	DT	25-NOV-2002 (first entry)	
XX	DE	Nucleotide sequence of a regulatory sequence for human CCR3.	
XX	KW	Human; CC chemokine receptor 3; CCR3; allergic disorder; probe;	
XX	KW	inflammatory disorder; eosinophil; hypersensitivity; leukemia;	
XX	KW	infectious disorder; HIV; respiratory syncytial virus infection; ss.	
XX	OS	Homo sapiens.	
XX	EH	Key	Location/Qualifiers
FT	misc_binding	24..27	
FT		/tag= a	
FT		/note= "transcription factor binding site for GATA"	
FT	misc_binding	40..43	
FT		/tag= b	
FT		/note= "transcription factor binding site for GATA"	
XX	XX	MO200262848-A2.	
XX	XX	15-AUG-2002.	
XX	XX	06-FEB-2002; 2002WO-US003442.	
XX	XX	07-FEB-2001; 2001US-0267073P.	
XX	XX	05-FEB-2002; 2002US-00068067.	
XX	XX	(CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.	
XX	XX	Rothenberg ME, Zimmerman N;	
XX	XX	WPI; 2002-657524/70.	
XX	XX	New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated	
XX	XX	exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable	
XX	XX	of binding to regulatory elements, useful for preventing e.g. allergic	
XX	XX	inflammatory reactions.	
XX	XX	Claim 2; Page 25; 56pp; English.	

CC The present sequence represents a probe for the human CC chemokine
 CC receptor 3 (CCR3) gene. The probe comprises +10 to +60 of exon 1 of CCR3,
 CC and is a regulatory sequence for CCR3. CCR3 is expressed on cells
 CC involved in allergic and/or inflammatory disorders. The gene comprises 4
 CC exons, with the coding region present on exon 4. The specification
 CC describes methods of regulating the expression of CCR3. The regulatory
 CC site is derived from an untranslated exon 1, exon 2, exon 3 or promoter
 CC of a human CCR3 gene. Regulating the expression of the chemokine receptor
 CC CCR3 is useful for preventing or treating disorders involving
 CC eosinophils, such as allergic inflammatory and hypersensitivity
 CC reactions, certain types of leukemia, and certain infectious disorders
 CC involving CCR3, e.g. HIV or respiratory syncytial virus infection.
 CC Expression and modulation of CCR3 is a useful tool in assessing
 CC eosinophil targeting and in regulating eosinophil-mediated reactions and
 CC diseases

XX Sequence 51 BP; 13 A; 12 C; 11 G; 15 T; 0 U; 0 Other;

Query Match 100.0%; Score 51; DB 6; Length 51;
 Best Local Similarity 100.0%; Pred. No. 7.9e-12;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACCACTGGTCTTCTTGCTATCCGGGCAAGAACTTATCGAATAACA 51
 Db 1 GGTACCACTGGTCTTCTTGCTATCCGGGCAAGAACTTATCGAATAACA 51

RESULT 2

ABQ78519
 ID ABQ78519 standard; RNA; 51 BP.

AC ABQ78519;

XX 25-NOV-2002 (first entry)

XX Nucleotide sequence of a regulatory sequence for human CCR3.

XX Human; CC chemokine receptor 3; CCR3; allergic disorder; probe;
 XX inflammatory disorder; eosinophil; hypersensitivity; leukemia;
 XX infectious disorder; HIV; respiratory syncytial virus infection; ss.

OS Homo sapiens.

XX WO200262848-A2.

XX 15-AUG-2002.

XX 06-FEB-2002; 2002WO-US003442.

XX 07-FEB-2001; 2001US-0267073P.

XX 05-FEB-2002; 2002US-00068067.

XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

XX Rothenberg ME, Zimmerman N;

XX WPI; 2002-657524/70.

XX New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated
 XX exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable
 XX of binding to regulatory elements, useful for preventing e.g. allergic
 XX inflammatory reactions.

XX Claim 7; Page 56; 56pp; English.

XX The present sequence represents a probe for the human CC chemokine
 CC receptor 3 (CCR3) gene. The probe is a regulatory sequence for CCR3. CCR3
 CC is expressed on cells involved in allergic and/or inflammatory disorders.
 CC The gene comprises 4 exons, with the coding region present on exon 4. The
 CC specification describes methods of regulating the expression of CCR3. The
 CC regulatory site is derived from an untranslated exon 1, exon 2, exon 3 or
 CC promoter of a human CCR3 gene. Regulating the expression of the chemokine
 CC receptor CCR3 is useful for preventing or treating disorders involving

CC eosinophils, such as allergic inflammatory and hypersensitivity
 CC reactions, certain types of leukemia, and certain infectious disorders
 CC involving CCR3, e.g. HIV or respiratory syncytial virus infection.
 CC Expression and modulation of CCR3 is a useful tool in assessing
 CC eosinophil targeting and in regulating eosinophil-mediated reactions and
 CC diseases

XX Sequence 51 BP; 13 A; 12 C; 11 G; 0 T; 15 U; 0 Other;

Query Match 100.0%; Score 51; DB 6; Length 51;

Best Local Similarity 70.6%; Pred. No. 7.9e-12;

Matches 36; Conservative 15; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACCACTGGTCTTCTTGCTATCCGGGCAAGAACTTATCGAATAACA 51
 Db 1 GGUACCAUGGUGUCUUGUGUUAUCCGGGCAAGAACTTATCGAATAACA 51

RESULT 3

ABQ78513
 ID ABQ78513 standard; DNA; 2895 BP.

XX AC ABQ78513;

XX 25-NOV-2002 (first entry)

XX Nucleotide sequence of the human CCR3 gene promoter.

XX Human; CC chemokine receptor 3; CCR3; allergic disorder;
 XX inflammatory disorder; eosinophil; hypersensitivity; leukemia;
 XX infectious disorder; HIV; respiratory syncytial virus infection;
 XX promoter; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
 XX misc_signal 1640..1645
 XX /*tag= a
 XX /note= "splice donor consensus site"

XX WO200262848-A2.
 XX 15-AUG-2002.

XX 06-FEB-2002; 2002WO-US003442.

XX 07-FEB-2001; 2001US-0267073P.

XX 05-FEB-2002; 2002US-00068067.

XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

XX Rothenberg ME, Zimmerman N;

XX WPI; 2002-657524/70.

XX New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated
 XX exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable
 XX of binding to regulatory elements, useful for preventing e.g. allergic
 XX inflammatory reactions.

XX Disclosure; Fig 4; 56pp; English.

XX The present sequence represents the promoter of the human CC chemokine
 CC receptor 3 (CCR3) gene. CCR3 is expressed on cells involved in allergic
 CC and/or inflammatory disorders. The gene comprises 4 exons, with the
 CC coding region present on exon 4. The specification describes methods of
 CC regulating the expression of CCR3. The regulatory site is derived from an
 CC untranslated exon 1, exon 2, exon 3 or promoter of a human CCR3 gene.
 CC Regulating the expression of the chemokine receptor CCR3 is useful for
 CC preventing or treating disorders involving eosinophils, such as allergic
 CC inflammatory and hypersensitivity reactions, certain types of leukemia,
 CC and certain infectious disorders involving CCR3, e.g. HIV or respiratory
 CC syncytial virus infection. Expression and modulation of CCR3 is a useful

CC tool in assessing eosinophil targeting and in regulating eosinophil-mediated reactions and diseases

XX Sequence 2895 BP; 829 A; 590 C; 556 G; 920 T; 0 U; 0 Other;

SQ

Query Match 100.0%; Score 51; DB 6; Length 2895;
 Best Local Similarity 100.0%; Pred. No. 2.4e-11;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACACATGGTCTTCTGTGCTTATCCGGCAAGAACTTATCGAATACA 51
 |||||
 Db 1561 GGTACACATGGTCTTCTGTGCTTATCCGGCAAGAACTTATCGAATACA 1611

RESULT 4
 AAT31335
 ID AAT31335 standard; cDNA; 1193 BP.

XX AAT31335;

XX 15-NOV-1996 (first entry)

XX CC-chemokine receptor 3 cDNA clone.

XX CC-chemokine receptor 3; CXR-3; Eos-L2; inhibitor; antisense;
 KW antiinflammatory; eosinophil; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH 92..1159
 FT CDS /*tag= a

FT variation

FT 918..919

FT /note= "CXR-3 cDNA clone has GC at positions 918-919,
 coding for serine (AGC) at position 276; a genomic clone
 has CG at these positions, coding for threonine (AGC)"

PN WO9623271-A2.

XX 25-JUL-1996.

XX 19-JAN-1996; 96WO-US000608.

XX 19-JAN-1995; 95US-00375199.

XX (LEUK-) LEUKOSITE INC.

PA (BGM) BRIGHAM & WOMENS HOSPITAL.

PA (CHIL-) CHILDRENS MEDICAL CENT.

PI Gerard CJ, Gerard NP, Mackay CR, Ponath PD, Post TW, Qin S;

DR WPI; 1996-354528/35.

P-PSDB; AAW03377.

XX Mammalian chemokine receptor-3 and related nucleic acids - useful to
 PT identify receptor inhibitors to treat inflammatory disease, e.g.
 PT autoimmune disorders, certain cancers, etc.

XX Claim 1; Page 111-113; 153pp; English.

XX A genomic DNA clone (AAT31335) codes for a novel receptor (AAW03377),
 CC designated Eos L2 or C-C chemokine receptor 3 (CXR-3), involved in
 CC leukocyte migration associated with inflammation. It was isolated from a
 CC human library constructed from eosinophils obtd. from a patient with
 CC hyper-eosinophilic syndrome using a probe (p4 cDNA) encoding the MIP-
 CC 1alpha/RANTES receptor. A CXR-3 genomic clone (AAT31334) was also
 CC isolated, and a consensus sequence is given in AAT31336. The cDNA and
 CC genomic clones can be used for the prodn. of recombinant CXR-3 in host
 CC cells, or to design antisense sequences useful for treating inflammatory
 CC disease

XX Sequence 1193 BP; 274 A; 310 C; 275 G; 334 T; 0 U; 0 Other;

Query Match 68.6%; Score 35; DB 2; Length 1193;
 Best Local Similarity 100.0%; Pred. No. 0.00013;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TTGTGCTTATCCGGCAAGAACTTATCGAATACA 51
 |||||
 Db 1 TTGTGCTTATCCGGCAAGAACTTATCGAATACA 35

RESULT 5

AAV07403
 ID AAV07403 standard; cDNA; 1193 BP.

XX AAV07403;

XX 28-SEP-1998 (first entry)

XX Human C-C chemokine receptor 3 cDNA.

XX C-C chemokine receptor 3; CXR-3; CCR3; Eos L2; human;
 KW G protein-coupled receptor; leukocyte; antibody; antagonist;
 KW inflammation; allergy; asthma; graft rejection; infection;
 KW autoimmune disease; drug screening; therapy; ds.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH 92..1159
 FT CDS /*tag= a

XX WO9814480-A1.

XX 09-APR-1998.

XX 24-SEP-1997; 97WO-US017103.

XX 30-SEP-1996; 96US-00720565.

XX (LEUK-) LEUKOSITE INC.

XX Mackay CR, Ponath PD;

XX WPI; 1998-286418/25.

XX P-PSDB; AAW51745.

XX Antibodies to chemokine receptor-3 protein - useful for diagnosis and
 PT treatment of inflammatory conditions, e.g. allergy, asthma, autoimmune
 PT disease, graft rejection or cancer.

XX Example 8; Page 134-136; 185pp; English.

XX This cDNA codes for novel human C-C chemokine receptor 3 (see AAW51745),
 CC also designated CXR-3, CCR3 or Eos L2, that binds and mediates chemotaxis
 CC in response to chemokines such as eotaxin, RANTES and MCP-3. The cDNA was
 CC isolated from a human eosinophil cDNA library constructed from
 CC eosinophils obtained from a patient with hypereosinophilic syndrome, and
 CC using CXR-1 cDNA as probe. A genomic DNA sequence (see AAV07402) is also
 CC provided as well as a consensus sequence (see AAV07404) for CXR-3. The
 CC invention relates to isolated and/or recombinant nucleic acids encoding
 CC CXR-3, isolated or recombinant CXR-3 polypeptides, recombinant CXR-3
 CC acid constructs, host cells useful for production of recombinant CXR-3
 CC proteins, to antibodies reactive with the receptors, and to methods of
 CC using these products to identify ligands, antagonists and agonists of
 CC receptor function. Inhibitors of CXR-3 can be used to treat: inflammatory
 CC or allergic diseases and conditions, including respiratory allergic
 CC diseases such as asthma, allergic rhinitis, hypersensitivity lung
 CC disease, hypersensitivity pneumonitis, eosinophilic pneumonia (e.g.
 CC Loeffler's syndrome, chronic eosinophilic pneumonia, interstitial lung
 CC disease (ILD) e.g. idiopathic pulmonary fibrosis or ILD associated with
 CC rheumatoid arthritis, systemic lupus erythematosus, ankylosing
 CC spondylitis, systemic sclerosis, Sjogren's syndrome, polymyositis or
 CC dermatomyositis), systemic anaphylaxis or hypersensitivity responses.

CC drug allergy, insect sting allergy, inflammatory bowel disease, such as
 CC Crohn's disease and ulcerative colitis, spondyloarthritis, scleroderma,
 CC psoriasis, inflammatory dermatosis such as dermatitis, eczema, atopic
 CC dermatitis, allergic contact dermatitis, urticaria, vasculitis (e.g.
 CC necrotizing, cutaneous and hypersensitivity vasculitis); eosinophilic
 CC myositis and eosinophilic fasciitis; autoimmune diseases such as
 CC rheumatoid arthritis, psoriatic arthritis, multiple sclerosis, systemic
 CC lupus erythematosus, myasthenia gravis, juvenile onset diabetes,
 CC glomerulonephritis, autoimmune thyroiditis and Behcet's disease; graft
 CC rejection, including allograft rejection or graft-versus-host disease;
 CC cancers with leukocyte infiltration of the skin or organs; and also
 CC reperfusion injury, atherosclerosis, certain haematologic malignancies,
 CC septic shock and endotoxic shock. Promoters of CKR-3 function can be used
 CC for treating: immunosuppression e.g. in AIDS patients or individuals
 CC undergoing radiation therapy, chemotherapy, therapy for autoimmune
 CC disease or other drug therapy, and immunosuppression due congenital
 CC deficiency in receptor function or other causes; and infectious diseases
 CC such as parasitic diseases, including helminth infections, such as
 CC nematodes (round worms). The agents can also be used for detection and
 CC diagnosis
 CC
 CC Sequence 1193 BP; 274 A; 310 C; 275 G; 334 T; 0 U; 0 Other;

Query Match 68.6%; Score 35; DB 2; Length 1193;

Best Local Similarity 100.0%; Pred. No. 0.00013;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TTGTGCTTATCCGGCAAGAACTTATCGAATACA 51

DB 1 TTGTGCTTATCCGGCAAGAACTTATCGAATACA 35

RESULT 6

ADA20738

ID ADA20738 standard; cDNA; 1342 BP.

XX AC ADA20738;

XX DT 20-NOV-2003 (first entry)

XX DE Wheat cDNA encoding a cytosine 5-methyltransferase #1.

XX KW ss; gene; plant; respiratory burst oxidase; Rboh; trna-mnm-s-U-MT;

XX KW chromomethylase; cytosine 5-methyltransferase; phospholipase D;

XX KW transcription factor IIF; asparaginyl tRNA transferase;

XX KW glutaminyl tRNA transferase; EDS1; adaptin AP50; adaptin alpha;

XX KW adaptin betas; stress resistance; quality grain improvement; starch;

XX KW herbicide.

OS Triticum aestivum.

XX US2003003471-A1.

XX PD 02-JAN-2003.

XX PF 19-FEB-2002; 2002US-00078770.

XX PR 12-JUL-1999; 99US-0143400P.

XX PR 12-JUL-1999; 99US-0143405P.

XX PR 12-JUL-1999; 99US-0143410P.

XX PR 13-SEP-1999; 99US-0153534P.

XX PR 01-OCT-1999; 99US-0157401P.

XX PR 15-OCT-1999; 99US-0159878P.

XX PR 22-OCT-1999; 99US-0161223P.

XX PR 11-JUL-2000; 2000US-00614188.

XX FA (FAMO/) FAMODU O O.

XX FA (MIAO/) MIAO G.

XX PA (SIMM/) SIMMONS C R.

XX PA (WENG/) WENG Z.

XX PA (CAHO/) CAHOON R E.

XX PA (SAKA/) SAKAI H.

XX PA (QUNZ/) QUN Z.

(THOR/) THORPE C J.

(FADE/) FADER G M.

(LIBB/) LI B.

PI Fancdu OO, Miao G, Simmons CR, Weng Z, Cahoon RE, Sakai H;

PI Qun Z, Thorpe CU, Fader GM, Li B;

XX WPI; 2003-311885/30.

XX P-PSDB; ADA20739.

DR New phospholipase D polypeptides and polynucleotides, useful for
 XX genetically and physically mapping the genes that they are part of, and
 XX subsequently in plant breeding for developing lines with the desired
 XX phenotypes.

PS Disclosure; Page 110; 189pp; English.

XX The invention relates to an isolated polynucleotide encoding a
 CC phospholipase D comprising a nucleotide sequence (encoding a polypeptide
 CC of at least 80 amino acids having at least 92% identity based on the
 CC Clustal method of alignment when compared to the proteins appearing as ID
 CC 120-134 (even numbers) or their complements. Also included are
 CC nucleotides encoding 98 plant proteins (comprising respiratory burst
 CC oxidases (Rboh), trna-mnm-s-U-MT, chromomethylases, cytosine 5-
 CC methyltransferases, phospholipase D, transcription factor IIF,
 CC asparaginyl tRNA transferases, glutaminyl tRNA transferases, EDS1 (not
 CC defined), adaptin AP50, adaptin alpha and adaptin betas), chimaeric
 CC genes, host cells comprising the chimaeras, a virus comprising the gene,
 CC the encoded phospholipase D proteins, a method of selecting an isolated
 CC polynucleotide that affects the level of expression of a phospholipase D
 CC polypeptide in a plant cell, a method of obtaining a nucleic acid
 CC fragment encoding a phospholipase D polypeptide, a method for positive
 CC selection of a transformed cell and a method of altering the level of
 CC expression of a phospholipase D in a host cell. The polynucleotides may
 CC be used as probes for genetically and physically mapping the genes that
 CC they are part of, and as markers for traits linked to those genes. Such
 CC information may be used in plant breeding to develop lines with the
 CC desired phenotypes. The nucleic acids are useful in creating transgenic
 CC plants in which the polypeptides are present at higher or lower levels
 CC than normal, in cell types or developmental stages in which they are not
 CC normally found, and which would alter the level of stress and disease
 CC resistance, enhancement of gene expression or transcription, quality
 CC grain improvement, or generation of novel starches in those cells. The
 CC polypeptides can be used as a target to facilitate design and/or
 CC identification of inhibitors of those enzymes that may be useful as
 CC herbicides. The present sequence is a cDNA encoding one of the 98
 CC proteins of the invention.

XX SQ Sequence 1342 BP; 351 A; 281 C; 340 G; 370 T; 0 U; 0 Other;

Query Match

Best Local Similarity 43.9%; Score 22.4; DB 7; Length 1342;

Matches 32; Conservative 66.7%; Pred. No. 34;

Mismatches 16; Indels 0; Gaps 0;

QY 4 ACCACTGCTCTTCTTGCTTATCCGGCAAGAACTTATCGAATACA 51

DB 352 AGCACTGCTGTTGGGCGCCCTTCCGTGCAATTAACCTGTAGATACA 399

RESULT 7

ADA20746

ID ADA20746 standard; cDNA; 1343 BP.

XX AC ADA20746;

XX DT 20-NOV-2003 (first entry)

XX DE Wheat cDNA encoding a cytosine 5-methyltransferase #3.

XX KW ss; gene; plant; respiratory burst oxidase; Rboh; trna-mnm-s-U-MT;

XX KW chromomethylase; cytosine 5-methyltransferase; phospholipase D;

XX KW transcription factor IIF; asparaginyl tRNA transferase;

XX KW glutaminyl tRNA transferase; EDS1; adaptin AP50; adaptin alpha;

XX KW

KW adaptin betas; stress resistance; quality grain improvement; starch;
KW herbicide.
XX
OS Tricum aestivum.
PN US2003003471-A1.
XX
XX 02-JAN-2003.
XX
XX 19-FEB-2002; 2002US-00078770.
XX
PR 12-JUL-1999; 99US-0143400P.
PR 12-JUL-1999; 99US-0143409P.
PR 12-JUL-1999; 99US-0143410P.
PR 13-SEP-1999; 99US-0153534P.
PR 01-OCT-1999; 99US-0157401P.
PR 15-OCT-1999; 99US-0159878P.
PR 22-OCT-1999; 99US-0161223P.
PR 11-JUL-2000; 2000US-00614188.
XX
XX (FAMO/) FAMODU O O.
PA (MIAO/) MIAO G.
PA (SIMW/) SIMMONS C R.
PA (WENG/) WENG Z.
PA (CAHO/) CAHOON R E.
PA (SAXA/) SAKAI H.
PA (QUNZ/) QUN Z.
PA (THOR/) THORPE C J.
PA (FADE/) FADER G M.
PA (LIBB/) LI B.
XX
PI Pamodu OO, Miao G, Simmons CR, Weng Z, Cahoon RE, Sakai H;
PI Qun Z, Thorpe CJ, Fader GM, Li B;
XX
XX WPI; 2003-311885/30.
DR P-PSDB; ADA20747.
XX
XX New phospholipase D polypeptides and polynucleotides, useful for
PT genetically and physically mapping the genes that they are part of, and
PT subsequently in plant breeding for developing lines with the desired
PT phenotypes.
XX
PS Disclosure; Page 115-116; 189pp; English.
XX
XX The invention relates to an isolated polynucleotide encoding a
CC phospholipase D comprising a nucleotide sequence (encoding a polypeptide
CC of at least 80 amino acids having at least 92% identity based on the
CC Clustal method of alignment when compared to the proteins appearing as ID
CC 120-134 (even numbers) or their complements. Also included are
CC nucleotides encoding 98 plant proteins (comprising respiratory burst
CC oxidases (Rboh), RNA-mmm-s-U-MT, chromomethylases, cytosine 5-
CC methyltransferases, phospholipase D, transcription factor 11r,
CC asparaginyl tRNA transferases, glutamyl tRNA transferases, EDS1 (not
CC defined), adaptin AP50, adaptin alphas and adaptin betas), chimaeric
CC genes, host cells comprising the chimaeras, a virus comprising the gene,
CC the encoded phospholipase D proteins, a method of selecting an isolated
CC polynucleotide that affects the level of expression of a phospholipase D
CC polypeptide in a plant cell, a method of obtaining a nucleic acid
CC fragment encoding a phospholipase D polypeptide, a method for positive
CC selection of a transformed cell and a method of altering the level of
CC expression of a phospholipase D in a host cell. The polynucleotides may
CC be used as probes for genetically and physically mapping the genes that
CC they are part of, and as markers for traits linked to those genes. Such
CC information may be used in plant breeding to develop lines with the
CC desired phenotypes. The nucleic acids are useful in creating transgenic
CC plants in which the polypeptides are present at higher or lower levels
CC than normal, in cell types or developmental stages in which they are not
CC normally found, and which would alter the level of stress and disease
CC resistance, enhancement of gene expression or transcription, quality
CC grain improvement, or generation of novel starches in those cells. The
CC polypeptides can be used as a target to facilitate design and/or
CC identification of inhibitors of those enzymes that may be useful as
CC herbicides. The present sequence is a cDNA encoding one of the 98

CC proteins of the invention.
XX
SQ Sequence 1343 BP; 351 A; 281 C; 340 G; 371 T; 0 U; 0 Other;
Query Match 43.9%; Score 22.4; DB 7; Length 1343;
Best Local Similarity 66.7%; Pred. No. 34;
Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
Qy 4 ACCACTGGTCTTCTTGTGCTTATCCGGGCGAGAACTATCGAATACA 51
Db 352 AGCACTGCTGGTGGGCGCTTTCCGTCGCAATACTGTTAGAGATACA 399
RESULT 8
AAH30283
ID AAH30283 standard; cDNA; 420 BP.
XX
AC AAH30283;
XX
DT 27-JUL-2001 (first entry)
XX
DE Human colon cancer cell line Kml2L4-A cDNA library derived sequence #217.
XX
KW Human; diagnosis; colon cancer; cancer; malignant; chromosome mapping;
KW detection; colon cancer cell line Kml2L4-A; ss.
XX
OS Homo sapiens.
XX
PN WO200018916-A2.
XX
PD 06-APR-2000.
XX
XX 23-SEP-1999; 99WO-US022226.
XX
PR 28-SEP-1998; 98US-0102161P.
PR 28-SEP-1998; 98US-0102150P.
PR 29-SEP-1998; 98US-0102380P.
PR 08-OCT-1998; 98US-0103815P.
PR 27-OCT-1998; 98US-0105877P.
XX
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
XX
XX Williams LT, Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger J;
PI Reinhard C, Giese K, Randazzo F, Kennedy GC, Pot D, Kassam A;
PI Lamson G, Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;
PI Leshkowitz D, Kita D, Garcia V, Jones LW, Stache-Crain B;
XX
XX WPI; 2000-293155/25.
XX
XX Polynucleotide library comprising 1079 defined sequences, useful in the
PT form of an array to detect cancer or susceptibility to cancer.
XX
XX Claim 1; Page 246; 502pp; English.
XX
XX The present invention describes a library of polynucleotides comprising
CC 1079 polynucleotide sequences (given in AAH30067 to AAH31145). Also described
CC are: (1) an isolated polynucleotide (I) having at least 90% identity to
CC one of the 1079 sequences; (2) a recombinant host cell containing (1);
CC (3) an isolated polypeptide (II) encoded by (1); (4) an antibody that
CC specifically binds to (II); (5) a vector comprising (1); and (6) a method
CC of detecting differentially expressed genes correlated with a cancerous
CC state of a mammalian cell comprising detecting a gene product encoded by
CC one of the 1079 sequences given in the specification. The polynucleotides
CC are used to monitor patients having (or susceptible) to cancer to detect
CC potentially malignant events at a molecular level before they are
CC detectable at a gross morphological level. The polynucleotides are also
CC useful for monitoring the efficacy of various therapies and preventive
CC interventions. Polynucleotide probes based on the disclosed sequences are
CC useful for chromosome mapping and detection of transcription levels. The
CC 1079 polynucleotide sequences were derived from a human colon cancer cell
CC line Kml2L4-A cDNA library
XX

SQ Sequence 420 BP; 113 A; 113 C; 100 G; 93 T; 0 U; 1 Other;
 Query Match 43.5%; Score 22.2; DB 3; Length 420;
 Best Local Similarity 77.1%; Pred. No. 30;
 Matches 27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 QY 5 CCACGTGCTCTTGTGCTTATCCGGCAAGAACT 39
 ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 207 CCACGGTCTTCTCTCTCTCTCCCAAGAAGAACT 241

RESULT 9

AAF74867
 ID AAF74867 standard; DNA; 1313 BP.

XX AC AAF74867;

XX DT 22-MAY-2001 (first entry)

XX DE Leishmania major PPG nucleotide sequence.

XX KW Human; hPPG-1; PPG; proteophosphoglycan; detection; ds.

XX OS Leishmania major.

XX PN CN1272542-A.

XX PD 08-NOV-2000.

XX PF 11-APR-2000; 2000CN-00115368.

XX PR 11-APR-2000; 2000CN-00115368.

XX PA (NANF-) NANFANG RES CENT STATE HUMAN GENE GROUP.

XX PI Li N, Xiao H, Kang B;

XX WPI; 2001-183595/19.

XX DR P-PSDB; AAB74609.

XX FT Human phosphoglycan protein and its coded sequence.

XX FS Example 2; Page 17-19; 22pp; Chinese.

XX CC The present invention describes a human proteophosphoglycan protein designated hPPG-1. Also describes are methods for the preparation and detection of hPPG-1. The present sequence encodes the Leishmania major PPG protein which is used in comparison with the hPPG-1 protein, in an example from the present invention

XX SQ Sequence 1313 BP; 194 A; 457 C; 367 G; 295 T; 0 U; 0 Other;

Query Match 43.5%; Score 22.2; DB 4; Length 1313;
 Best Local Similarity 69.8%; Pred. No. 41;
 Matches 30; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 4 ACCACTGCTCTTGTGCTTATCCGGCAAGAACTATCGAA 46
 ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 878 ACCACAGCACTTCTCTGGTGATATATCAAGAACTACTCGAA 920

RESULT 10

ABK73357
 ID ABK73357 standard; DNA; 1719 BP.

XX AC ABK73357;

XX DT 13-AUG-2002 (first entry)

XX DE Bacillus licheniformis genomic sequence tag (GST) #648.

XX KW Differential gene expression; genomic sequenced tag; GST;

XX KW altered culture condition; environmental stress;

KW physiological provocation; ds.
 XX Bacillus licheniformis.
 XX WC200229113-A2.
 XX PD 11-APR-2002.
 XX PF 05-OCT-2001; 2001WO-US031437.
 XX PR 06-OCT-2000; 2000US-00680598.
 XX PR 27-MAR-2001; 2001US-0279526P.
 XX PA (NOVO) NOVOZYMES BIOTECH INC.
 XX PA (NOVO) NOVOZYMES AS.
 XX PI Berka R, Clausen IG;
 XX WPI; 2002-416684/44.
 XX PT Monitoring differential expression of several genes in first Bacillus cell relative to expression of same genes in one or more second Bacillus cells, by using substrate containing Bacillus genomic sequenced tag array.
 XX PS Claim 4; SEQ ID NO 648; 200pp; English.

XX CC The invention describes a method of monitoring differential expression of genes in a first Bacillus cell relative to expression of the genes in other Bacillus cells, comprising hybridising labelled nucleic acid probes isolated from Bacillus cells to a substrate containing array of Bacillus genomic sequenced tags (GST), examining the array, and determining relative gene expression by an observed hybridisation reporter signal of a spot in the array. The method is useful for measuring the expression of genes in a first Bacillus cell relative to expression of the same genes in one or more second Bacillus cells. The method is useful for monitoring global expression of several genes from a Bacillus cell, discovering new genes, identifying possible functions of unknown open reading frames and monitoring gene copy number variation and stability. Monitoring changes in expression of genes may be used to provide a representation of the way in which Bacillus cells adapt to changes in culture conditions, environmental stress or other physiological provocation. Extensive follow-up characterisation is unnecessary, when one spot on an array equals one gene or one open reading frame, since sequence information is available. This sequence represents a genomic sequence tag (GST) used in the method of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 1719 BP; 530 A; 375 C; 413 G; 401 T; 0 U; 0 Other;

Query Match 43.5%; Score 22.2; DB 6; Length 1719;
 Best Local Similarity 77.1%; Pred. No. 44;
 Matches 27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 13 CTTCTTGCTTATCCGGCAAGAACTTATCGAAA 47
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 Db 1120 CTTCTGCTGCTTCTCGGCAAGTACATATCGAAA 1154

RESULT 11

AAS62217
 ID AAS62217 standard; cDNA; 1861 BP.

XX AC AAS62217;

XX DT 14-FEB-2002 (first entry)

XX DE cDNA sequence #4 encoding novel human secreted protein.

XX KW Human secreted protein; hyperproliferative disorder; autoimmune disorder;
 KW immune deficiency disorder; blood disorder; inflammatory disorder;
 KW infectious disorder; gene therapy; antimicrobial; hepatotropic;

PR 27-SEP-2000; 2000US-0235836P.
 PR 29-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 02-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239935P.
 PR 13-OCT-2000; 2000US-0239937P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241221P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241786P.
 PR 20-OCT-2000; 2000US-0241787P.
 PR 20-OCT-2000; 2000US-0241808P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 01-NOV-2000; 2000US-0241826P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 08-NOV-2000; 2000US-0246474P.
 PR 08-NOV-2000; 2000US-0246475P.
 PR 08-NOV-2000; 2000US-0246476P.
 PR 08-NOV-2000; 2000US-0246477P.
 PR 08-NOV-2000; 2000US-0246478P.
 PR 08-NOV-2000; 2000US-0246523P.
 PR 08-NOV-2000; 2000US-0246524P.
 PR 08-NOV-2000; 2000US-0246525P.
 PR 08-NOV-2000; 2000US-0246526P.
 PR 08-NOV-2000; 2000US-0246527P.
 PR 08-NOV-2000; 2000US-0246528P.
 PR 08-NOV-2000; 2000US-0246532P.
 PR 08-NOV-2000; 2000US-0246609P.
 PR 08-NOV-2000; 2000US-0246610P.
 PR 08-NOV-2000; 2000US-0246611P.
 PR 08-NOV-2000; 2000US-0246613P.
 PR 17-NOV-2000; 2000US-0249207P.
 PR 17-NOV-2000; 2000US-0249208P.
 PR 17-NOV-2000; 2000US-0249209P.
 PR 17-NOV-2000; 2000US-0249210P.
 PR 17-NOV-2000; 2000US-0249211P.
 PR 17-NOV-2000; 2000US-0249212P.
 PR 17-NOV-2000; 2000US-0249213P.
 PR 17-NOV-2000; 2000US-0249214P.
 PR 17-NOV-2000; 2000US-0249215P.
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 PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
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 PR 17-NOV-2000; 2000US-0249247P.
 PR 17-NOV-2000; 2000US-0249257P.
 PR 17-NOV-2000; 2000US-0249259P.
 PR 17-NOV-2000; 2000US-0249300P.
 PR 01-DEC-2000; 2000US-0250160P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-02559678P.
 (HUMA-) HUMAN GENOME SCI INC.
 PA XX
 XX XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-488783/53.
 DR P-FSDB; AAU16102.
 XX
 PT New nucleic acid molecules encoding 461 human secreted proteins for
 PT diagnosing, preventing, treating or ameliorating medical conditions and
 PT used as food additives or preservatives.
 XX
 XX Claim 1; SEQ ID NO 268; 980pp; English.
 XX
 CC The invention relates to isolated nucleic acid molecules and their
 CC encoded secreted proteins. The nucleic acids and proteins are used to
 CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
 CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
 CC in diagnosing a pathological condition or susceptibility to a
 CC pathological condition. Antibodies to the proteins can also be used in
 CC alleviating symptoms associated with the disorders and in diagnostic
 CC immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays
 CC (ELISA). Disorders which are diagnosed or treated include autoimmune
 CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.
 CC neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac
 CC arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiodysplasia,
 CC nervous system disorders e.g. Alzheimer's disease, infections caused by
 CC bacteria, viruses and fungi and ocular disorders e.g. corneal infection,
 CC and many other disorders listed in the specification. The polypeptides
 CC can also be used to aid wound healing and epithelial cell proliferation,
 CC to prevent skin aging due to sunburn, to maintain organs before
 CC transplantation, for supporting cell culture of primary tissues, to
 CC regenerate tissues and in chemotaxis. The polypeptides can also be used
 CC as a food additive or preservative to increase or decrease storage
 CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
 CC minerals, cofactors and other nutritional components. The present
 CC sequence encodes a novel secreted protein of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 Query Match 43.5%; Score 22.2; DB 4; Length 2102;
 Best Local Similarity 77.1%; Pred. No. 46;
 Matches 27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 QY 5 CCACGGGCTTCTTCTGCTTATCCGGGCAAGAACT 39
 |||||
 Db 1104 CCACGGGCTTCTTCTTCTTCTTCTTCCAGCAAGAACT 1138
 |||||
 RESULT 13
 AEX73430
 ID ABX73430 standard; DNA; 2102 BP.
 XX
 AC ABX73430;
 XX
 DT 18-MAR-2003 (first entry)
 XX
 DE Human novel polynucleotide #258.
 XX
 KW Human; gene; ds; neural disorder; immune system disorder; renal disorder;
 KW muscular disorder; respiratory disease; reproductive disorder;
 KW gastrointestinal disorder; pulmonary disorder; cardiovascular disorder;
 KW hyperproliferative disorder; inflammatory disease; allergic reaction;
 KW blood related disorder; cancer; immunosuppressive; antiinflammatory;
 KW cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic;
 KW haemostatic; antiarteriosclerotic.
 XX
 OS Homo sapiens.
 XX
 XX US2002132753-A1.
 PN
 XX 19-SEP-2002.
 PD
 XX 17-JAN-2001; 2001US-00764864.
 PF
 XX 31-JAN-2000; 2000US-0179065P.
 PR
 XX 04-FEB-2000; 2000US-0180628P.
 PR

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OM nucleic - nucleic search, using sw model
Run on: August 2, 2004, 19:08:00 ; Search time 111.328 Seconds
968.934 Million cell updates/sec

Title: US-10-068-067-17

Perfect score: 22

Sequence: 1 ggtaccactggtctctgtgc 22

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Gapop 60.0 , Gapext 60.0

Searched: 3222919 seqs, 245157024 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6445838

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:

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- 6: /cgn2_6/ptodata/1/pubpna/ECTUS_PUBCOMB.seq*
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- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq*
- 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2*
- 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq*
- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq*
- 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq*
- 17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq*
- 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq*
- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	22	100.0	51	14	Sequence 17, Appl
3	22	100.0	51	14	Sequence 16, Appl
4	22	100.0	2895	14	Sequence 21, Appl
5	21	95.5	21	14	Sequence 11, Appl
6	15	68.2	695	13	Sequence 22, Appl
7	15	68.2	695	13	Sequence 114054,
8	15	68.2	695	13	Sequence 114055,
9	15	68.2	695	16	Sequence 114056,
10	15	68.2	695	16	Sequence 114057,
11	15	68.2	695	16	Sequence 114058,
C 12	15	68.2	767	13	Sequence 114059, A
C 13	15	68.2	767	13	Sequence 14404, A
C 14	15	68.2	767	13	Sequence 145338,
C 15	68.2	767	13	US-10-027-632-145339	Sequence 145339,

C 15	68.2	767	13	US-10-027-632-145340	Sequence 145340, A
C 16	68.2	767	16	US-10-027-632-14404	Sequence 14404, A
C 17	68.2	767	16	US-10-027-632-145338	Sequence 145338,
C 18	68.2	767	16	US-10-027-632-145339	Sequence 145339,
C 19	68.2	767	16	US-10-027-632-145340	Sequence 145340, A
C 20	68.2	1251	15	US-10-198-846-13243	Sequence 13243, A
C 21	68.2	1267	13	US-10-372-876-78	Sequence 78, Appl
C 22	68.2	1267	13	US-10-097-065-78	Sequence 78, Appl
C 23	68.2	1335	17	US-10-425-114-2891	Sequence 2891, Ap
C 24	68.2	1335	17	US-10-437-963-25606	Sequence 25606, A
C 25	68.2	1335	17	US-10-437-963-89665	Sequence 89665, A
C 26	68.2	2895	17	US-10-437-963-89667	Sequence 89667, A
C 27	68.2	2895	17	US-10-027-632-112371	Sequence 112371,
C 28	68.2	3261	16	US-10-027-632-112371	Sequence 112371,
C 29	68.2	109201	17	US-10-450-826-32	Sequence 32, Appl
C 30	68.2	118067	15	US-10-081-327-32	Sequence 232, App
C 31	68.2	228139	13	US-10-081-327-32	Sequence 232, App
C 32	68.2	25	17	US-10-717-597-2928	Sequence 2928, App
C 33	68.2	60	10	US-09-908-975-5528	Sequence 5528, Ap
C 34	68.2	255	17	US-10-437-963-30581	Sequence 30581, A
C 35	68.2	359	17	US-10-469-285-438	Sequence 438, App
C 36	68.2	390	13	US-10-424-599-11913	Sequence 11913, A
C 37	68.2	390	10	US-09-918-995-16250	Sequence 16250, A
C 38	68.2	400	10	US-09-918-995-4377	Sequence 4377, Ap
C 39	68.2	453	17	US-10-437-963-45777	Sequence 45777, A
C 40	68.2	468	9	US-09-864-761-2123	Sequence 2123, Ap
C 41	68.2	479	13	US-10-027-632-292457	Sequence 292457,
C 42	68.2	479	16	US-10-027-632-292457	Sequence 292457,
C 43	68.2	542	15	US-10-255-536-135	Sequence 135, App
C 44	68.2	545	13	US-09-770-152-602	Sequence 602, App
C 45	68.2	559	13	US-10-027-632-223556	Sequence 223556,

ALIGNMENTS

RESULT 1
US-10-068-067-17
; Sequence 17, Application US/10068067
; Publication No. US20020151064A1
; GENERAL INFORMATION:
; APPLICANT: Rothenberg, Marc E.
; APPLICANT: Zimmermann, Nives
; APPLICANT: Children's Hospital Medical Center
; TITLE OF INVENTION: REGULATION OF CCR3 EXPRESSION
; FILE REFERENCE: CMC-153
; CURRENT APPLICATION NUMBER: US/10/068,067
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 60/267,073
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 17
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-068-067-17

Query Match 100.0%; Score 22; DB 14; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.0065; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0;
QY 1 GGTACCACTGGTCTCTGTGC 22
Db 1 GGTACCACTGGTCTCTGTGC 22
RESULT 2
US-10-068-067-16
; Sequence 16, Application US/10068067
; Publication No. US20020151064A1
; GENERAL INFORMATION:
; APPLICANT: Rothenberg, Marc E.

; APPLICANT: Zimmermann, Nives
; APPLICANT: Children's Hospital Medical Center
; TITLE OF INVENTION: REGULATION OF CCR3 EXPRESSION
; FILE REFERENCE: CMC-153
; CURRENT APPLICATION NUMBER: US/10/068,067
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 60/267,073
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-068-067-16

Query Match 100.0%; Score 22; DB 14; Length 51;
Best Local Similarity 100.0%; Pred. No. 0.006;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACCACTGGTCTTCTGTGC 22
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Db 1 GGTACCACTGGTCTTCTGTGC 22

RESULT 3
US-10-068-067-21
; Sequence 21, Application US/10068067
; Publication No. US20020151064A1
; GENERAL INFORMATION:
; APPLICANT: Rothenberg, Marc E.
; APPLICANT: Zimmermann, Nives
; APPLICANT: Children's Hospital Medical Center
; TITLE OF INVENTION: REGULATION OF CCR3 EXPRESSION
; FILE REFERENCE: CMC-153
; CURRENT APPLICATION NUMBER: US/10/068,067
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 60/267,073
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 51
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-068-067-21

Query Match 100.0%; Score 22; DB 14; Length 51;
Best Local Similarity 63.6%; Pred. No. 0.006;
Matches 14; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACCACTGGTCTTCTGTGC 22
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Db 1 GGUACCACUGGUCUUCUGGC 22

RESULT 4
US-10-068-067-11
; Sequence 11, Application US/10068067
; Publication No. US20020151064A1
; GENERAL INFORMATION:
; APPLICANT: Rothenberg, Marc E.
; APPLICANT: Zimmermann, Nives
; APPLICANT: Children's Hospital Medical Center
; TITLE OF INVENTION: REGULATION OF CCR3 EXPRESSION
; FILE REFERENCE: CMC-153
; CURRENT APPLICATION NUMBER: US/10/068,067
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 60/267,073
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11

; LENGTH: 2895
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-068-067-11

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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1561 GGTACCACTGGTCTTCTGTGC 1582

RESULT 5
US-10-068-067-22
; Sequence 22, Application US/10068067
; Publication No. US20020151064A1
; GENERAL INFORMATION:
; APPLICANT: Rothenberg, Marc E.
; APPLICANT: Zimmermann, Nives
; APPLICANT: Children's Hospital Medical Center
; TITLE OF INVENTION: REGULATION OF CCR3 EXPRESSION
; FILE REFERENCE: CMC-153
; CURRENT APPLICATION NUMBER: US/10/068,067
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 60/267,073
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 24
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; LENGTH: 21
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-068-067-22

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QY 1 GGTACCACTGGTCTTCTGTG 21
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RESULT 6
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; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114054


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; LENGTH: 695
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-114054

Query Match      68.2%; Score 15; DB 13; Length 695;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACTGGTCTTCTTG 21
Db 464 ACTGGTCTTCTTG 478

RESULT 7
US-10-027-632-114055
; Sequence 114055, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
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; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114055
; LENGTH: 695
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-114055

Query Match      68.2%; Score 15; DB 13; Length 695;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACTGGTCTTCTTG 21
Db 464 ACTGGTCTTCTTG 478

RESULT 8
US-10-027-632-114056
; Sequence 114056, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
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; LENGTH: 695
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-114055

Query Match      68.2%; Score 15; DB 13; Length 695;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACTGGTCTTCTTG 21
Db 464 ACTGGTCTTCTTG 478

RESULT 9
US-10-027-632-114054
; Sequence 114054, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114054
; LENGTH: 695
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-114054

Query Match      68.2%; Score 15; DB 13; Length 695;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACTGGTCTTCTTG 21
Db 464 ACTGGTCTTCTTG 478

RESULT 10
US-10-027-632-114055
; Sequence 114055, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
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; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114056
; LENGTH: 695
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-114056

Query Match      68.2%; Score 15; DB 13; Length 695;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACTGGTCTTCTTG 21
Db 464 ACTGGTCTTCTTG 478

RESULT 9
US-10-027-632-114054
; Sequence 114054, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114054
; LENGTH: 695
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-114054

Query Match      68.2%; Score 15; DB 16; Length 695;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACTGGTCTTCTTG 21
Db 464 ACTGGTCTTCTTG 478

RESULT 10
US-10-027-632-114055
; Sequence 114055, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
```

;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;; FILE REFERENCE: 108827.129
;; CURRENT APPLICATION NUMBER: US/10/027,632
;; CURRENT FILING DATE: 2002-04-30

;; PRIOR APPLICATION NUMBER: US 60/218,006
;; PRIOR FILING DATE: 2000-07-12
;; PRIOR APPLICATION NUMBER: US 60/198,676
;; PRIOR FILING DATE: 2000-04-20
;; PRIOR APPLICATION NUMBER: US 60/193,483
;; PRIOR FILING DATE: 2000-03-29
;; PRIOR APPLICATION NUMBER: US 60/185,218
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/167,363
;; PRIOR FILING DATE: 1999-11-23
;; PRIOR APPLICATION NUMBER: US 60/156,358
;; PRIOR FILING DATE: 1999-09-28
;; PRIOR APPLICATION NUMBER: US 60/146,002
;; PRIOR FILING DATE: 1999-08-09
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 114055
;; LENGTH: 695
;; TYPE: DNA
;; ORGANISM: Human
US-10-027-632-114055

Query Match 68.2%; Score 15; DB 15; Length 695;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACTGGTCTCTTGTG 21
| | | | | | | | | |
Db 464 ACTGGTCTCTTGTG 478

RESULT 11

US-10-027-632-114055
;; Sequence 114056, Application US/10027632
;; Publication No. US20030204075A9
;; GENERAL INFORMATION:
;; APPLICANT: Wang, David G.
;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;; FILE REFERENCE: 108827.129
;; CURRENT APPLICATION NUMBER: US/10/027,632
;; CURRENT FILING DATE: 2002-04-30
;; PRIOR APPLICATION NUMBER: US 60/218,006
;; PRIOR FILING DATE: 2000-07-12
;; PRIOR APPLICATION NUMBER: US 60/198,676
;; PRIOR FILING DATE: 2000-04-20
;; PRIOR APPLICATION NUMBER: US 60/193,483
;; PRIOR FILING DATE: 2000-03-29
;; PRIOR APPLICATION NUMBER: US 60/185,218
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/167,363
;; PRIOR FILING DATE: 1999-11-23
;; PRIOR APPLICATION NUMBER: US 60/156,358
;; PRIOR FILING DATE: 1999-09-28
;; PRIOR APPLICATION NUMBER: US 60/146,002
;; PRIOR FILING DATE: 1999-08-09
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 114056
;; LENGTH: 695
;; TYPE: DNA
;; ORGANISM: Human
US-10-027-632-114056

Query Match 68.2%; Score 15; DB 16; Length 695;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACTGGTCTCTTGTG 21
| | | | | | | | | |
Db 464 ACTGGTCTCTTGTG 478

RESULT 12

US-10-027-632-14404/c
;; Sequence 14404, Application US/10027632
;; Publication No. US20020198371A1
;; GENERAL INFORMATION:
;; APPLICANT: Wang, David G.
;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;; FILE REFERENCE: 108827.129
;; CURRENT APPLICATION NUMBER: US/10/027,632
;; CURRENT FILING DATE: 2002-04-30
;; PRIOR APPLICATION NUMBER: US 60/218,006
;; PRIOR FILING DATE: 2000-07-12
;; PRIOR APPLICATION NUMBER: US 60/198,676
;; PRIOR FILING DATE: 2000-04-20
;; PRIOR APPLICATION NUMBER: US 60/193,483
;; PRIOR FILING DATE: 2000-03-29
;; PRIOR APPLICATION NUMBER: US 60/185,218
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/167,363
;; PRIOR FILING DATE: 1999-11-23
;; PRIOR APPLICATION NUMBER: US 60/156,358
;; PRIOR FILING DATE: 1999-09-28
;; PRIOR APPLICATION NUMBER: US 60/146,002
;; PRIOR FILING DATE: 1999-08-09
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 14404
;; LENGTH: 767
;; TYPE: DNA
;; ORGANISM: Human
US-10-027-632-14404

Query Match 68.2%; Score 15; DB 13; Length 767;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ACCACTGGTCTTCTT 18
| | | | | | | | | |
Db 628 ACCACTGGTCTTCTT 614

RESULT 13

US-10-027-632-145338/c
;; Sequence 145338, Application US/10027632
;; Publication No. US20020198371A1
;; GENERAL INFORMATION:
;; APPLICANT: Wang, David G.
;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;; FILE REFERENCE: 108827.129
;; CURRENT APPLICATION NUMBER: US/10/027,632
;; CURRENT FILING DATE: 2002-04-30
;; PRIOR APPLICATION NUMBER: US 60/218,006
;; PRIOR FILING DATE: 2000-07-12
;; PRIOR APPLICATION NUMBER: US 60/198,676
;; PRIOR FILING DATE: 2000-04-20
;; PRIOR APPLICATION NUMBER: US 60/193,483
;; PRIOR FILING DATE: 2000-03-29
;; PRIOR APPLICATION NUMBER: US 60/185,218
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/167,363
;; PRIOR FILING DATE: 1999-11-23
;; PRIOR APPLICATION NUMBER: US 60/156,358
;; PRIOR FILING DATE: 1999-09-28
;; PRIOR APPLICATION NUMBER: US 60/146,002
;; PRIOR FILING DATE: 1999-08-09
;; NUMBER OF SEQ ID NOS: 325720

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 145338
; LENGTH: 767
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-145338

Query Match 68.2%; Score 15; DB 13; Length 767;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ACCACTGGTCTTCTT 18
|||
Db 628 ACCACTGGTCTTCTT 614

RESULT 14

US-10-027-632-145339/c
; Sequence 145339, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome

; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/10/027,632

; CURRENT FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: US 60/218,006

; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483

; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: US 60/185,218

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002

; PRIOR FILING DATE: 1999-08-09

; NUMBER OF SEQ ID NOS: 325720

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 145339

; LENGTH: 767

; TYPE: DNA

; ORGANISM: Human

US-10-027-632-145339

Query Match 68.2%; Score 15; DB 13; Length 767;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ACCACTGGTCTTCTT 18
|||
Db 628 ACCACTGGTCTTCTT 614

RESULT 15

US-10-027-632-145340/c
; Sequence 145340, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome

; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/10/027,632

; CURRENT FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: US 60/218,006

; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 145340
; LENGTH: 767
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-145340

Query Match 68.2%; Score 15; DB 13; Length 767;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ACCACTGGTCTTCTT 18
|||
Db 628 ACCACTGGTCTTCTT 614

Search completed: August 2, 2004, 22:36:35
Job time : 112.328 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 16:56:38 ; Search time 106.207 Seconds
(without alignments)
879.984 Million cell updates/sec

Title: US-10-068-067-17

Perfect score: 22

Sequence: 1 ggtaccactgggtcttctgtgc 22

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N Geneseq_29Jan04.*

- 1: geneseqn1980s.*
- 2: geneseqn1980s.*
- 3: geneseqn2000s.*
- 4: geneseqn2000s.*
- 5: geneseqn2000s.*
- 6: geneseqn2000s.*
- 7: geneseqn2000s.*
- 8: geneseqn2000s.*
- 9: geneseqn2000s.*
- 10: geneseqn2000s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	22	ABQ78515	Abq78515 Nucleotid
2	22	100.0	51	ABQ78514	Abq78514 Nucleotid
3	22	100.0	51	ABQ78519	Abq78519 Nucleotid
4	22	100.0	2895	ABQ78513	Abq78513 Nucleotid
5	21	95.5	21	ABQ78520	Abq78520 Nucleotid
6	16	72.7	406	ABQ78520	Abq78520 Nucleotid
7	15	68.2	240	ABQ78520	Abq78520 Nucleotid
8	15	68.2	249	ABQ78520	Abq78520 Nucleotid
9	15	68.2	278	ABQ78520	Abq78520 Nucleotid
10	15	68.2	700	ABQ78520	Abq78520 Nucleotid
11	15	68.2	700	ABQ78520	Abq78520 Nucleotid
12	15	68.2	823	ABQ78520	Abq78520 Nucleotid
13	15	68.2	1076	ABQ78520	Abq78520 Nucleotid
14	15	68.2	1078	ABQ78520	Abq78520 Nucleotid
15	15	68.2	1267	ABQ78520	Abq78520 Nucleotid
16	15	68.2	1267	ABQ78520	Abq78520 Nucleotid
17	15	68.2	2000	ABQ78520	Abq78520 Nucleotid
18	15	68.2	5046	ABQ78520	Abq78520 Nucleotid
19	15	68.2	5450	ABQ78520	Abq78520 Nucleotid
20	15	68.2	109201	ABQ78520	Abq78520 Nucleotid
21	14	63.6	22	ABQ78520	Abq78520 Nucleotid
22	14	63.6	31	ABQ78520	Abq78520 Nucleotid
23	14	63.6	60	ABQ78520	Abq78520 Nucleotid

ALIGNMENTS

RESULT 1

ABQ78515
ID ABQ78515 standard; DNA; 22 BP.
XX AC ABQ78515;
XX DT 25-NOV-2002 (first entry)
XX DE Nucleotide sequence of a regulatory sequence for human CCR3.
XX KW Human; CC chemokine receptor 3; CCR3; allergic disorder; probe;
XX KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;
XX KW infectious disorder; HIV; respiratory syncytial virus infection; ss.
XX OS Homo sapiens.
XX FN WO200262848-A2.
XX PD 15-AUG-2002.
XX PF 06-FEB-2002; 2002WO-US003442.
XX PR 07-FEB-2001; 2001US-0267073P.
XX PR 05-FEB-2002; 2002US-00068067.
(CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Rothenberg WE, Zimmerman N;
WPI; 2002-657524/70.
New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated
exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable
of binding to regulatory elements, useful for preventing e.g. allergic
inflammatory reactions.
Claim 6; Page 54; 56pp; English.
The present sequence represents a probe for the human CC chemokine
receptor 3 (CCR3) gene. The probe is a regulatory sequence for CCR3. CCR3
is expressed on cells involved in allergic and/or inflammatory disorders.
The gene comprises 4 exons, with the coding region present on exon 4. The
specification describes methods of regulating the expression of CCR3. The
regulatory site is derived from an untranslated exon 1, exon 2, exon 3 or
promoter of a human CCR3 gene. Regulating the expression of the chemokine
receptor CCR3 is useful for preventing or treating disorders involving

24 14 63.6 359 4 AAK53873 Murine re
25 14 63.6 378 5 AAF64835 Novel hum
26 14 63.6 392 8 ACH29038 Human adu
27 14 63.6 400 8 ACH17165 Human adu
28 14 63.6 468 4 AAI12202 Probe #21
29 14 63.6 468 4 ABA53909 Human foe
30 14 63.6 468 4 AAI33552 Probe #22
31 14 63.6 468 4 ABA43455 Human bre
32 14 63.6 468 4 ABA23657 Probe #21
33 14 63.6 468 4 AAK27622 Human bon
34 14 63.6 468 4 AAK02175 Human bra
35 14 63.6 468 4 ABA27192 Human liv
36 14 63.6 468 5 AAI02114 Probe #21
37 14 63.6 468 6 ABA02085 Human gen
38 14 63.6 521 4 AAK89500 Human dig
39 14 63.6 537 4 ABA87976 Human d9
40 14 63.6 540 5 ABA48958 Human pro
41 14 63.6 542 5 AAS05535 Mammalian
42 14 63.6 545 7 ABA57250 Arabidops
43 14 63.6 568 3 AAC34694 Arabidops
44 14 63.6 600 4 AAD11098 Human cal
45 14 63.6 601 3 AAF11306 Aspergill

CC eosinophils, such as allergic inflammatory and hypersensitivity
 CC reactions, certain types of leukemia, and certain infectious disorders
 CC involving CCR3, e.g. HIV or respiratory syncytial virus infection.
 CC Expression and modulation of CCR3 is a useful tool in assessing
 CC eosinophil targeting and in regulating eosinophil-mediated reactions and
 CC diseases
 XX
 SQ Sequence 22 BP; 2 A; 6 C; 6 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 6; Length 22;
 Best Local Similarity 100.0%; Pred. NO. 0.017;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACCACTGGTCTCTTGTC 22
 |||||
 DB 1 GGTACCACTGGTCTCTTGTC 22

RESULT 2
 ABQ78514
 ID ABQ78514 standard; DNA; 51 BP.
 XX
 AC ABQ78514;
 XX
 DT 25-NOV-2002 (first entry)
 XX
 DE Nucleotide sequence of a regulatory sequence for human CCR3.

Human; CC chemokine receptor 3; CCR3; allergic disorder; probe;
 inflammatory disorder; eosinophil; hypersensitivity; leukemia;
 infectious disorder; HIV; respiratory syncytial virus infection; ss.
 XX
 OS Homo sapiens.

Key Location/Qualifiers
 XX misc_binding 24..27
 FT /*tag= a
 FT /note= "transcription factor binding site for GATA"
 FT misc_binding 40..43
 FT /*tag= b
 FT /note= "transcription factor binding site for GATA"
 XX
 PN WO200262848-A2.
 XX
 PD 15-AUG-2002.

XX 06-FEB-2002; 2002WO-US003442.
 XX 07-FEB-2001; 2001US-0267073P.
 PR 05-FEB-2002; 2002US-00068067.
 XX
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 XX
 PI Rothenberg ME, Zimmerman N;
 XX WPI; 2002-657524/70.
 XX
 DR
 XX
 PT New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated
 PT exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable
 PT of binding to regulatory elements, useful for preventing e.g. allergic
 PT inflammatory reactions.
 XX
 XX Claim 2; Page 25; 56pp; English.

XX The present sequence represents a probe for the human CC chemokine
 CC receptor 3 (CCR3) gene. The probe comprises +10 to +60 of exon 1 of CCR3,
 CC and is a regulatory sequence for CCR3. CCR3 is expressed on cells
 CC involved in allergic and/or inflammatory disorders. The gene comprises 4
 CC exons, with the coding region present on exon 4. The specification
 CC describes methods of regulating the expression of CCR3. The regulatory
 CC site is derived from an untranslated exon 1, exon 2, exon 3 or promoter
 CC of a human CCR3 gene. Regulating the expression of the chemokine receptor
 CC CCR3 is useful for preventing or treating disorders involving

CC eosinophils, such as allergic inflammatory and hypersensitivity
 CC reactions, certain types of leukemia, and certain infectious disorders
 CC involving CCR3, e.g. HIV or respiratory syncytial virus infection.
 CC Expression and modulation of CCR3 is a useful tool in assessing
 CC eosinophil targeting and in regulating eosinophil-mediated reactions and
 CC diseases
 XX
 SQ Sequence 51 BP; 13 A; 12 C; 11 G; 15 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 6; Length 51;
 Best Local Similarity 100.0%; Pred. NO. 0.017;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACCACTGGTCTCTTGTC 22
 |||||
 DB 1 GGTACCACTGGTCTCTTGTC 22

RESULT 3
 ABQ78519
 ID ABQ78519 standard; RNA; 51 BP.
 XX
 AC ABQ78519;
 XX
 DT 25-NOV-2002 (first entry)
 XX
 DE Nucleotide sequence of a regulatory sequence for human CCR3.

Human; CC chemokine receptor 3; CCR3; allergic disorder; probe;
 inflammatory disorder; eosinophil; hypersensitivity; leukemia;
 infectious disorder; HIV; respiratory syncytial virus infection; ss.
 XX
 OS Homo sapiens.

PN WO200262848-A2.
 XX
 PD 15-AUG-2002.
 XX 06-FEB-2002; 2002WO-US003442.
 XX 07-FEB-2001; 2001US-0267073P.
 PR 05-FEB-2002; 2002US-00068067.
 XX
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 XX
 PI Rothenberg ME, Zimmerman N;
 XX WPI; 2002-657524/70.

XX New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated
 XX exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable
 XX of binding to regulatory elements, useful for preventing e.g. allergic
 XX inflammatory reactions.
 XX
 XX Claim 7; Page 56; 56pp; English.

XX The present sequence represents a probe for the human CC chemokine
 CC receptor 3 (CCR3) gene. The probe is a regulatory sequence for CCR3. CCR3
 CC is expressed on cells involved in allergic and/or inflammatory disorders.
 CC The gene comprises 4 exons, with the coding region present on exon 4. The
 CC specification describes methods of regulating the expression of CCR3. The
 CC regulatory site is derived from an untranslated exon 1, exon 2, exon 3 or
 CC promoter of a human CCR3 gene. Regulating the expression of the chemokine
 CC receptor CCR3 is useful for preventing or treating disorders involving
 CC eosinophils, such as allergic inflammatory and hypersensitivity
 CC reactions, certain types of leukemia, and certain infectious disorders
 CC involving CCR3, e.g. HIV or respiratory syncytial virus infection.
 CC Expression and modulation of CCR3 is a useful tool in assessing
 CC eosinophil targeting and in regulating eosinophil-mediated reactions and
 CC diseases

XX Sequence 51 BP; 13 A; 12 C; 11 G; 15 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 6; Length 51;
 Best Local Similarity 63.6%; Pred. No. 0.017; 0; Indels 0; Gaps 0;
 Matches 14; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGATACCACTGGTCTCTTGTGC 22
 |||||
 Db 1561 GGATACCACTGGTCTCTTGTGC 1582

RESULT 5
 ABQ78520
 ID ABQ78520 standard; RNA; 21 BP.
 XX AC ABQ78520;
 XX DT 25-NOV-2002 (first entry)
 XX DE Nucleotide sequence of a regulatory sequence for human CCR3.
 XX KW Human; CC chemokine receptor 3; CCR3; allergic disorder; probe;
 XX KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;
 XX KW infectious disorder; HIV; respiratory syncytial virus infection; ss.
 XX OS Homo sapiens.
 XX PN WO200262848-A2.
 XX PD 15-AUG-2002.
 XX PF 06-FEB-2002; 2002WO-US003442.
 XX PR 07-FEB-2001; 2001US-0267073P.
 XX PR 05-FEB-2002; 2002US-00068067.
 XX PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 XX PI Rothenberg ME, Zimmerman N;
 XX DR WPI; 2002-657524/70.
 XX PT New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated
 PT exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable
 PT of binding to regulatory elements, useful for preventing e.g. allergic
 PT inflammatory reactions.
 XX PS Claim 8; Page 56; 56pp; English.

XX The present sequence represents a probe for the human CC chemokine
 CC receptor 3 (CCR3) gene. The probe is a regulatory sequence for CCR3. CCR3
 CC is expressed on cells involved in allergic and/or inflammatory disorders.
 CC The gene comprises 4 exons, with the coding region present on exon 4. The
 CC specification describes methods of regulating the expression of CCR3. The
 CC regulatory site is derived from an untranslated exon 1, exon 2, exon 3 or
 CC promoter of a human CCR3 gene. Regulating the expression of the chemokine
 CC receptor CCR3 is useful for preventing or treating disorders involving
 CC eosinophils, such as allergic inflammatory and hypersensitivity
 CC reactions, certain types of leukemia, and certain infectious disorders
 CC involving CCR3, e.g. HIV or respiratory syncytial virus infection.
 CC Expression and modulation of CCR3 is a useful tool in assessing
 CC eosinophil targeting and in regulating eosinophil-mediated reactions and
 CC diseases
 XX Sequence 21 BP; 2 A; 5 C; 6 G; 0 T; 8 U; 0 Other;
 SQ Query Match 95.5%; Score 21; DB 6; Length 21;
 Best Local Similarity 61.9%; Pred. No. 0.06;
 Matches 13; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGATACCACTGGTCTCTTGTGC 21
 |||||
 Db 1 GGATACCACTGGTCTCTTGTGC 21

RESULT 6
 ADB51450/c
 ID ADB51450 standard; DNA; 406 BP.
 XX

Query Match 100.0%; Score 22; DB 6; Length 2895;
 Best Local Similarity 100.0%; Pred. No. 0.046; 0; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AC ADB51450;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:1992.
 XX
 KW toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;
 KW toxicity marker; toxicity progression; drug screening;
 KW primary rat hepatocyte toxicity modelling; gene; ds.
 XX
 OS Rattus norvegicus.
 XX
 FN WO2003065993-A2.
 XX
 FD 14-AUG-2003.
 XX
 PF 04-FEB-2003; 2003WO-US003482.
 XX
 PR 04-FEB-2002; 2002US-0353171P.
 PR 13-MAR-2002; 2002US-0363534P.
 PR 08-APR-2002; 2002US-0370248P.
 PR 10-APR-2002; 2002US-0371134P.
 PR 10-APR-2002; 2002US-0371135P.
 PR 10-APR-2002; 2002US-0371150P.
 PR 11-APR-2002; 2002US-0371413P.
 PR 13-APR-2002; 2002US-0373601P.
 PR 19-APR-2002; 2002US-0373602P.
 PR 22-APR-2002; 2002US-0374139P.
 PR 08-MAY-2002; 2002US-0378370P.
 PR 09-MAY-2002; 2002US-0378652P.
 PR 09-MAY-2002; 2002US-0378653P.
 PR 09-MAY-2002; 2002US-0378655P.
 PR 09-JUL-2002; 2002US-0394230P.
 PR 09-JUL-2002; 2002US-0394253P.
 PR 04-SEP-2002; 2002US-0407688P.
 PR 28-JAN-2003; 2003US-0442900P.
 XX
 PA (GENE-) GENE LOGIC INC.
 XX
 XX Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Orr M;
 PI Elashoff M;
 XX
 XX WPI; 2003-731472/69.
 XX
 DR Determining if a compound induces a toxic effect on a tissue or cell, for
 PT identifying hepatotoxic compounds, comprises comparing a gene expression
 PT profile of a tissue or cell sample to a database of Tox mean and non-Tox
 PT mean values.
 XX
 XX Claim 44; SEQ ID NO 1992; 874pp; English.
 PS
 XX The present invention describes a method for determining whether a
 CC compound induces a toxic effect on a tissue or cell. The method comprises
 CC preparing a gene expression profile of a tissue or cell sample exposed to
 CC the compound, and comparing the gene expression profile to a database
 CC comprising data or information on the Tox mean and non-Tox mean value.
 CC The method is useful for predicting or identifying at least one toxic
 CC effect, particularly hepatotoxicity, of a test or unknown compound. The
 CC genes listed in the specification are useful as diagnostic or toxicity
 CC markers for the prediction or identification of the physiological state
 CC of tissue or cell sample that has been exposed to a compound, or to
 CC identify or predict the toxic effects of a compound or an agent. These
 CC may also be used as markers for monitoring toxicity progression or for
 CC drug screening. The present sequence represents a primary rat hepatocyte
 CC toxicity modelling related gene sequence from the present invention.
 XX
 XX Sequence 406 BP; 130 A; 95 C; 87 G; 94 T; 0 U; 0 Other;
 SQ
 Query Match 72.7%; Score 16; DB 9; Length 406;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 6 CACTGGTCTCTTG 21

DB 129 CACTGGTCTCTTG 114
 |||||
 RESULT 7
 AAA61159/c
 ID AAA61159 standard; DNA; 240 BP.
 AC AAA61159;
 XX
 DT 12-OCT-2000 (first entry)
 XX
 DE SEN virus genome fragment SEQ ID NO: 116.
 XX
 KW SEN virus; SENV; gastrointestinal tract disorder; inflammatory disease;
 KW proliferative disorder; hepatopathy; hepatitis; viral infection;
 KW vaccination; gene therapy; ds.
 XX
 OS Hepatitis virus.
 XX
 FN WO200028039-A2.
 XX
 PD 18-MAY-2000.
 XX
 PF 09-NOV-1999; 99WO-EP008566.
 XX
 PR 10-NOV-1998; 98IT-MI002437.
 PR 30-APR-1999; 99IT-MI000923.
 PR 14-MAY-1999; 99EP-00830298.
 PR 16-JUL-1999; 99EP-00113932.
 XX
 PA (DIAS-) DIASORIN SRL.
 XX
 PI Primi D, Fiordalisi G, Mantero GL, Mattioli S, Sottini A;
 PI Bonelli F, Vaglini L, Olivero P, Dal Corso A, Bonelli M;
 XX
 XX WPI; 2000-376551/32.
 XX
 DR Nucleic acids representing the genome of the SEN virus (SENV) and encoded
 PT proteins, useful for treatment of hepatopathies, inflammatory diseases
 PT and proliferative disorders such as cancer.
 XX
 PS Claim 1; Page 353; 392pp; English.
 XX
 CC The present invention is concerned with the sequence of the genome of the
 CC SEN virus (SENV), and the proteins encoded by it. SENV is thought to be
 CC the cause of hepatopathies which are not linked to the presence of the
 CC hepatitis A, B and E viruses in man. The genome and proteins of this
 CC virus can be used in gene therapy and vaccination against the virus,
 CC which also causes disorders of the gastrointestinal tract, including
 CC Crohn's disease and lupus erythematosus, inflammatory diseases, and
 CC proliferative disorders such as cancer
 XX
 SQ Sequence 240 BP; 70 A; 57 C; 46 G; 67 T; 0 U; 0 Other;
 Query Match 68.2%; Score 15; DB 3; Length 240;
 Best Local Similarity 100.0%; Pred. No. 99;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 GTACCACTGGTCTTC 16
 |||||
 DB 28 GTACCACTGGTCTTC 14
 |||||
 RESULT 8
 ABB16387/c
 ID ABB16387 standard; cDNA; 249 BP.
 XX
 AC ABB16387;
 XX
 DT 24-JUN-2002 (first entry)
 XX
 DE Human ORFX polynucleotide sequence SEQ ID NO:1251.

XX Human, open reading frame; ORFX; gene therapy; cancer; cirrhosis;
 KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
 KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
 KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
 KW hypertension; hypothyroidism; cholesterol ester storage disease;
 KW immune deficiency; immune disorder; infectious disease;
 KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
 KW myasthenia gravis; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200192523-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 29-MAY-2001; 2001WO-US010836.
 XX
 PR 30-MAY-2000; 2000US-0206132P.
 PR 29-AUG-2000; 2000US-0228716P.
 XX
 PA (CURA-) CUPAGEN CORP.
 XX
 XX Shinkets RA, Leach MD;
 PI WPI; 2002-106308/14.
 DR P-PSDB; ABP00635.
 DR
 XX Novel human polypeptides and polynucleotides useful for diagnosing,
 PT preventing and treating cardiovascular disease, neurodegenerative,
 PT hyperproliferative disorders and autoimmune disorders.
 XX
 PS Disclosure; SEQ ID NO 1251; 1037pp; English.
 XX
 CC The present invention describes substantially purified human proteins
 CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
 CC in the specification). ABN5762 to ASN27252 encode the human ORFX
 CC proteins given in ABP0010 to ABP11500. ORFX proteins are useful for
 CC treating or preventing a pathology associated with an ORFX-associated
 CC disorder in humans, and in the manufacture of a medicament for treating a
 CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
 CC sequences can be used in gene therapy. ORFX sequences can be used in the
 CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
 CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
 CC osteoarthritis, neurodegenerative disorders, disorders related to organ
 CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
 CC lupus erythematosus, hyperextension, hypothyroidism, cholesterol ester
 CC storage disease, various immune deficiencies and disorders, infectious
 CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
 CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
 CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
 CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
 CC bone degenerative disorders, or periodontal disease, and for gut
 CC protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues and conditions resulting from
 CC systemic cytotoxic damage. N.B. The sequence data for this patent did not
 CC form part of the printed specification, but was obtained in electronic
 CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 249 BP; 60 A; 58 C; 74 G; 57 T; 0 U; 0 Other;
 Query Match 68.2%; Score 15; DB 6; Length 249;
 Best Local Similarity 100.0%; Pred. No. 99;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 TACCACCTGGTCTTC 17
 DB 38 TACCACCTGGTCTTC 24
 RESULT 9
 AAA61168/c
 ID AAA61168 standard; DNA; 278 BP.

XX AAA61168;
 AC 12-OCT-2000 (first entry)
 DT SEN virus genome fragment SEQ ID NO: 177.
 DE SEN virus; SENV; gastrointestinal tract disorder; inflammatory disease;
 KW proliferative disorder; hepatopathy; hepatitis; viral infection;
 KW vaccination; gene therapy; ds.
 XX
 OS Hepatitis virus.
 XX
 PN WO2000028039-A2.
 XX
 PD 18-MAY-2000.
 XX
 PF 09-NOV-1999; 99WO-EP008566.
 XX
 PR 10-NOV-1998; 98IT-MI002437.
 PR 30-APR-1999; 99IT-MI000923.
 PR 14-MAY-1999; 99EP-00830298.
 PR 16-JUL-1999; 99EP-00113932.
 XX
 PA (DIAS-) DIASORIN SRL.
 XX
 PI Primi D, Fiordalisi G, Mantero GL, Mattioli S, Sottini A;
 PI Bonelli F, Vaglini L, Olivero P, Dal Corso A, Bonelli M;
 DR WPI; 2000-376551/32.
 XX
 PT Nucleic acids representing the genome of the SEN virus (SENV) and encoded
 PT proteins, useful for treatment of hepatopathies, inflammatory diseases
 PT and proliferative disorders such as cancer.
 XX
 PS Claim 1; Page 371; 392pp; English.
 XX
 CC The present invention is concerned with the sequence of the genome of the
 CC SEN virus (SENV), and the proteins encoded by it. SENV is thought to be
 CC the cause of hepatopathies which are not linked to the presence of the
 CC hepatitis A, B and E viruses in man. The genome and proteins of this
 CC virus can be used in gene therapy and vaccination against the virus,
 CC which also causes disorders of the gastrointestinal tract, including
 CC Crohn's disease and lupus erythematosus, inflammatory diseases, and
 CC proliferative disorders such as cancer
 XX
 SQ Sequence 278 BP; 83 A; 67 C; 53 G; 75 T; 0 U; 0 Other;
 Query Match 68.2%; Score 15; DB 3; Length 278;
 Best Local Similarity 100.0%; Pred. No. 99;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GTACCACCTGGTCTTC 16
 DB 28 GTACCACCTGGTCTTC 14
 RESULT 10
 AAH92754
 ID AAH92754 standard; DNA; 700 BP.
 XX
 AC AAH92754;
 XX
 DT 09-OCT-2001 (first entry)
 XX
 DE Human inflammatory bowel disease related gene fragment IGR3079a.
 XX
 KW Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
 KW chromosome 5q31-33; forensic test; gene therapy; ds.
 XX
 OS Homo sapiens.
 XX

PN WO200142511-A2.
 XX 14-JUN-2001.
 XX PF 11-DEC-2000; 2000WO-US033632.
 XX PR 10-DEC-1999; 99US-0170257P.
 XX PR 10-APR-2000; 2000US-0196046P.
 XX (WHED) WHITEHEAD INST BIOMEDICAL RES.
 XX PA (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
 XX PI Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;
 XX DR WPI; 2001-367874/38.
 XX
 XX Testing for the presence of polymorphisms associated with inflammatory
 XX bowel disease, using a hybridization assay.
 XX
 XX Disclosure; Page 304-305; 463pp; English.
 XX
 XX The present invention describes a method for detecting the presence of
 XX polymorphisms associated with inflammatory bowel diseases such as
 XX ulcerative colitis and Crohn's disease. The methods can be used to detect
 XX the presence of genetic polymorphisms associated with inflammatory bowel
 XX disease and correlating their occurrence with disease states. They may be
 XX used in this way for phenotypic correlations, forensics, paternity
 XX testing, medicine and genetic analysis. The present sequence is a gene
 XX containing a polymorphic site described in the exemplification of the
 XX invention
 XX
 XX SQ Sequence 700 BP; 183 A; 184 C; 148 G; 185 T; 0 U; 0 Other;
 XX
 XX Query Match 68.2%; Score 15; DB 4; Length 700;
 XX Best Local Similarity 100.0%; Pred. No. 97;
 XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 6 CACTGGCTCTCTTGT 20
 XX 14 CACTGGCTCTCTTGT 28
 XX DB
 XX
 XX RESULT 11
 XX AAH92753
 XX ID AAH92753 standard; DNA; 700 BP.
 XX AC AAH92753;
 XX DT 09-OCT-2001 (first entry)
 XX DE Human inflammatory bowel disease related gene fragment IGR3078a.
 XX KW Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 XX KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
 XX KW chromosome 5q31-33; forensic test; gene therapy; ds.
 XX OS Homo sapiens.
 XX PN WO200142511-A2.
 XX PD 14-JUN-2001.
 XX PF 11-DEC-2000; 2000WO-US033632.
 XX PR 10-DEC-1999; 99US-0170257P.
 XX PR 10-APR-2000; 2000US-0196046P.
 XX (WHED) WHITEHEAD INST BIOMEDICAL RES.
 XX PA (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
 XX PI Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;
 XX DR WPI; 2001-367874/38.
 XX

XX Testing for the presence of polymorphisms associated with inflammatory
 XX bowel disease, using a hybridization assay.
 XX
 XX Disclosure; Page 304; 463pp; English.
 XX
 XX The present invention describes a method for detecting the presence of
 XX polymorphisms associated with inflammatory bowel diseases such as
 XX ulcerative colitis and Crohn's disease. The methods can be used to detect
 XX the presence of genetic polymorphisms associated with inflammatory bowel
 XX disease and correlating their occurrence with disease states. They may be
 XX used in this way for phenotypic correlations, forensics, paternity
 XX testing, medicine and genetic analysis. The present sequence is a gene
 XX containing a polymorphic site described in the exemplification of the
 XX invention
 XX
 XX SQ Sequence 700 BP; 179 A; 197 C; 173 G; 151 T; 0 U; 0 Other;
 XX
 XX Query Match 68.2%; Score 15; DB 4; Length 700;
 XX Best Local Similarity 100.0%; Pred. No. 97;
 XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 6 CACTGGCTCTCTTGT 20
 XX 514 CACTGGCTCTCTTGT 528
 XX DB
 XX
 XX RESULT 12
 XX ABV10808/c
 XX ID ABV10808 standard; CDNA; 823 BP.
 XX AC ABV10808;
 XX DT 13-SEP-2002 (first entry)
 XX DE Human prostate expression marker cDNA 10799.
 XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 XX KW pharmacogenomic marker; gene; ss.
 XX OS Homo sapiens.
 XX PN WO200160860-A2.
 XX PD 23-AUG-2001.
 XX PF 20-FEB-2001; 2001WO-US005171.
 XX PR 17-FEB-2000; 2000US-0183319P.
 XX PR 16-MAR-2000; 2000US-0189862P.
 XX PR 25-MAY-2000; 2000US-0207454P.
 XX PR 09-JUN-2000; 2000US-0211314P.
 XX PR 18-JUL-2000; 2000US-0219007P.
 XX PR 13-DEC-2000; 2000US-0255281P.
 XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 XX Schlegel R, Endege WO, Monahan JE;
 XX WPI; 2001-662795/76.
 XX
 XX Novel isolated nucleic acid molecule associated with cancerous state of
 XX prostate cells and correlating with presence of prostate cancer, useful
 XX for detecting presence of prostate cancer, stage of prostate cancer.
 XX
 XX Claim 1; Page 1746; 11750pp; English.
 XX
 XX The invention relates to an isolated nucleic acid molecule (I) comprising
 XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 XX specification or its complement. (I) is useful for: (a) assessing whether
 XX a patient is afflicted with prostate cancer; (b) monitoring the
 XX progression of prostate cancer in a patient; (c) assessing the efficacy
 XX of a test compound to inhibit prostate cancer in a patient; (d) assessing

CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
SQ Sequence 823 BP; 299 A; 162 C; 201 G; 160 T; 0 U; 1 Other;

Query Match 68.2%; Score 15; DB 5; Length 823;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGGCTTCTTCTGC 22
Db 717 CTGGCTTCTTCTGC 703

RESULT 13

AAC45720
ID AAC45720 standard; DNA; 1076 BP.

XX AC AAC45720;

XX DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 47521.

KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-00301439.

XX PR 25-FEB-1999; 99US-0121825P.

XX PR 05-MAR-1999; 99US-0121802P.

XX PR 09-MAR-1999; 99US-0123548P.

XX PR 23-MAR-1999; 99US-0125788P.

XX PR 25-MAR-1999; 99US-0126264P.

XX PR 29-MAR-1999; 99US-0126785P.

XX PR 01-APR-1999; 99US-0127462P.

XX PR 06-APR-1999; 99US-0128234P.

XX PR 08-APR-1999; 99US-0128714P.

XX PR 16-APR-1999; 99US-0128845P.

XX PR 19-APR-1999; 99US-0130077P.

XX PR 21-APR-1999; 99US-0130449P.

XX PR 23-APR-1999; 99US-0130510P.

XX PR 28-APR-1999; 99US-0130891P.

XX PR 30-APR-1999; 99US-0131444P.

XX PR 30-APR-1999; 99US-0132048P.

XX PR 04-MAY-1999; 99US-0132407P.

XX PR 05-MAY-1999; 99US-0132484P.

XX PR 06-MAY-1999; 99US-0132486P.

XX PR 06-MAY-1999; 99US-0132487P.

XX PR 07-MAY-1999; 99US-0132863P.

XX PR 11-MAY-1999; 99US-0134256P.

XX PR 14-MAY-1999; 99US-0134218P.

XX PR 14-MAY-1999; 99US-0134219P.

XX PR 14-MAY-1999; 99US-0134221P.

XX PR 14-MAY-1999; 99US-0134370P.

XX PR 18-MAY-1999; 99US-0134370P.

XX PR 19-MAY-1999; 99US-0134768P.

XX PR 20-MAY-1999; 99US-0134941P.

XX PR 20-MAY-1999; 99US-0135124P.

XX PR 21-MAY-1999; 99US-0135353P.

XX PR 24-MAY-1999; 99US-0135629P.

XX PR 25-MAY-1999; 99US-0136021P.

PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139452P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140831P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144684P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 03-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.

PR	23-OCT-1999;	99US-01621412B.
Query Match	68.2%;	
Best Local Similarity	100.0%;	
Matches	15;	Conservative
Qy	3	TACCACTGGCTCTCT 17
Db	279	TACCACTGGCTCTCT 293
RESULT 14		
AAC41924		
ID	AAC41924	standard; DNA; 1078
XX	AAC41924;	
XX	AC	
XX	AC	
XX	DT	17-OCT-2000 (first entry)
XX		
DE	Arabidopsis thaliana	DNA frag
XX		
KW	Hybridisation assay; genetic	
KW	protein identification; signal	
KW	promoter; termination sequenc	
XX		
OS	Arabidopsis thaliana.	
XX		
XX	EP1033405-A2.	
XX		
PD	06-SEP-2000.	
XX		
XX		
PP	25-FEB-2000;	20C0EP-003014139.
PR	25-FEB-1999;	99US-0121825P.
PR	03-MAR-1999;	99US-0123180P.
PR	09-MAR-1999;	99US-0123548P.
PR	23-MAR-1999;	99US-0125788P.
PR	25-MAR-1999;	99US-0126264P.
PR	29-MAR-1999;	99US-0126785P.
PR	01-APR-1999;	99US-0127462P.
PR	06-APR-1999;	99US-0128234P.
PR	08-APR-1999;	99US-0128714P.
PR	16-APR-1999;	99US-0129845P.
PR	19-APR-1999;	99US-0130077P.
PR	21-APR-1999;	99US-0130449P.
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KW protein identification; signal		
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Db 279 TACCACTGGTCTTCT 293
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DT 17-SEP-1999 (first entry)
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KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
KW digestive disorder; endocrine disorder; infection; AIDS; ss.
XX
OS Homo sapiens.
XX
EN WO931117-A1.
XX
PD 24-JUN-1999.
XX
PF 17-DEC-1998; 98WO-US027059.
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PR 18-DEC-1997; 97US-0068006P.
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PR 18-DEC-1997; 97US-0070923P.
PR 18-DEC-1997; 97US-0068169P.
PR 19-DEC-1997; 97US-0068365P.
PR 19-DEC-1997; 97US-0068367P.
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XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Moore PA, Ruben SM, Carter KC, Shi Y, Rosen CA, Soppet DR;
PI Kyaw H, Wei Y, Florence K, Duan RD, Florence C, Greene JM, Feng P;
PI Perrie AM, Yu G, Janat F, Ni J;
XX
DR WPI; 1999-418749/35.
DR P-PSDB; AAY36286.
XX
PT New isolated human genes encoding secreted polypeptides.
XX
PS Claim 1; Page 309; 537pp; English.
XX
CC AAX97916 to AAX98029 represent 110 isolated human secreted protein genes.
CC AAY36224 to AAY36727 represent the secreted proteins encoded by the 110
CC human genes. The genes and their corresponding secreted polypeptides are
CC useful for preventing, treating or ameliorating medical conditions, e.g.
CC by protein or gene therapy. Also pathological conditions can be diagnosed
CC by determining the amount of the new polypeptides in a sample or by
CC determining the presence of mutations in the new genes. Specific uses are
CC described for each of the 110 genes, based on which tissues they are most
CC highly expressed in, and include developing products for the diagnosis or
CC treatment of cancer, tumours, developmental abnormalities and foetal
CC deficiencies, blood disorders, diseases of the immune system, autoimmune
CC diseases, inflammation, allergies, Alzheimer's and cognitive disorders,
CC schizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders,
CC atherosclerosis, diabetes, cardiovascular disorders, kidney disorders,
CC digestive/endocrine disorders, infections and AIDS. The polypeptides are
CC also useful for identifying their binding partners. The sequences given
CC in AAX97907 to AAX97915 and AAY36223 are used in the exemplification of

CC the present invention
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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18	18	81.8	436	9	AF262304	Homo sapi
19	18	81.8	173554	2	AC144357	Danio rer
20	17	77.3	5883	2	AC129517	Homo sapi
21	17	77.3	112182	2	AC141177	Rattus no
22	17	77.3	114458	10	BX293986	Mouse DNA
23	17	77.3	161846	9	AL358532	Human DNA
24	17	77.3	172834	2	AC135133	Rattus no
25	17	77.3	172834	2	AC011277	Homo sapi
26	17	77.3	196769	2	AC120900	Rattus no
27	17	77.3	204102	2	AC013826	Homo sapi
28	17	77.3	202220	2	AC125657	Rattus no
29	17	77.3	229200	2	AC106425	Rattus no
30	17	77.3	235201	2	AC114470	Rattus no
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33	17	77.3	264110	2	AC122626	Rattus no
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41	16	72.7	146575	2	AC135571	Rattus no
42	16	72.7	152908	10	AC130550	Mus muscu
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ALIGNMENTS

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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

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Sequence 17 from Patent WO02062848.
AX513218
AX513218.1 GI:23504281
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Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1
Rothenberg, M.E. and Zimmerman, N.
Regulation of cc chemokine receptor 3 (ccr3) expression
Patent: WO 02062848-A 17 15-AUG-2002;
JOURNAL

AX513218
22 bp
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linear
PAT 03-OCT-2002

CHILDREN'S HOSPITAL MEDICAL CENTER (US)

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DEFINITION Sequence 16 from Patent WO02062848.

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VERSION AX513217.1 GI:23504280

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SOURCE Homo sapiens

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REFERENCE

1 Rothenberg M.E. and Zimmerman N.
AUTHORS Regulation of cc chemokine receptor 3 (ccr3) expression
TITLE Patent: WO 02062848-A 16 15-AUG-2002;
JOURNAL CHILDREN'S HOSPITAL MEDICAL CENTER (US)

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DEFINITION Sequence 21 from Patent WO02062848.

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SOURCE Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 Rothenberg M.E. and Zimmerman N.
AUTHORS Regulation of cc chemokine receptor 3 (ccr3) expression
TITLE Patent: WO 02062848-A 21 15-AUG-2002;
JOURNAL CHILDREN'S HOSPITAL MEDICAL CENTER (US)

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Best Local Similarity 100.0%; Pred. No. 0.021; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GGTACCACTGGTCTTCTTGTC 22

RESULT 4

AF262299 AF262299 348 bp mRNA linear PRI 26-JUN-2002
LOCUS Homo sapiens clone 1 CC chemokine receptor 3 (CCR3) mRNA, partial cds.

ACCESSION AF262299
VERSION AF262299.1 GI:19171640

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (Bases 1 to 348)
AUTHORS Vijh, S., Dayhoff, D.E., Wang, C.E., Imam, Z., Ehrenberg, P.K. and Michael, N.L.

TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence for a Rare TATA-less Promoter Structure Conserved between Drosophila and Humans

JOURNAL Genomics 80 (1), 86-95 (2002)
MEDLINE 22074933
PUBMED 12079287

REFERENCE

2 (Bases 1 to 348)
AUTHORS Vijh, S., Dayhoff, D.E., Wang, C.E., Ehrenberg, P.K. and Michael, N.L.

TITLE Direct Submission
JOURNAL Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis, Walter Reed Army Institute of Research, 1600 E. Gude Drive, Rockville, MD 20850, USA

FEATURES

source
Location/Qualifiers
1..348
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="3"
/map="3p21"
/clone="1"
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1..>348
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120..>348
/gene="CCR3"

gene

CDS

/note="G-protein coupled receptor; principal eotaxin receptor expressed on eosinophils, CD4 Th2 lymphocytes, CD8 lymphocytes, microglia, dendritic cells, and monocytes"

/codon_start=1

/product="CC chemokine receptor 3"

/protein_id="AAU85628.1"

/db_xref="GI:19171641"

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Best Local Similarity 100.0%; Pred. No. 0.017; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACCACTGGTCTTCTTGTC 22
DB 27 GGTACCACTGGTCTTCTTGTC 48

RESULT 5

AF224496S1 AF224496S1 957 bp DNA linear PRI 02-MAY-2001
LOCUS Homo sapiens CC chemokine receptor 3 (CCR3) gene, exon 1.

ACCESSION AF224496
 VERSION AF224496.1 GI:13924485
 KEYWORDS
 SEGMENT 1 of 2
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 957)
 AUTHORS Scotet,E.J.
 TITLE CCR3 expression is associated with chromatin remodeling in Th2 cells
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 957)
 AUTHORS Scotet,E.J.
 TITLE Direct Submission
 JOURNAL Submitted (13-JAN-2000) Basel Institute for Immunology, 487
 Grenzachstrasse, Basel CH-4005, Switzerland
 FEATURES
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 1..957
 /organism="Homo sapiens"
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 /note="exon 1"
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 Best Local Similarity 100.0%; Pred.No.0.016;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGTACCACTGGTCTTCTGTGC 22
 |||||
 DB 295 GGTACCACTGGTCTTCTGTGC 316
 |||||
 RESULT 6
 AF247360 1453 bp DNA linear PRI 26-JUN-2002
 LOCUS Homo sapiens CC chemokine receptor 3 (CCR3) gene, promoter region
 DEFINITION and partial sequence.
 ACCESSION AF247360
 VERSION AF247360.1 GI:19110541
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1453)
 AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and Michael,N.L.
 TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence for a Rare TATA-less Promoter Structure Conserved between Drosophila and Humans
 JOURNAL Genomics 80 (1), 86-95 (2002)
 MEDLINE 22074933
 PUBMED 12079287
 REFERENCE 2 (bases 1 to 1453)
 AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
 TITLE Direct Submission
 JOURNAL Submitted (21-MAR-2000) Dept. of Mol. Diag. and Pathogenesis, U.S. Military HIV Research Program, 1600 E. Gude Drive, Rockville, MD 20850, USA
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 /chromosome="3"
 /map="3p21; between CCR1 and CCR5"
 /clone="A8"
 /cell_type="peripheral blood mononuclear cell"

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 755
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 822..>1453
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 822..1163
 /gene="CCR3"
 1114
 /gene="CCR3"
 /replace="g"
 ORIGIN
 Query Match 100.0%; Score 22; DB 9; Length 1453;
 Best Local Similarity 100.0%; Pred.No.0.015; 0; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0;
 QY 1 GGTACCACTGGTCTTCTGTGC 22
 |||||
 DB 1082 GGTACCACTGGTCTTCTGTGC 1103
 |||||
 RESULT 7
 AF247359 1454 bp DNA linear PRI 26-JUN-2002
 LOCUS Homo sapiens CC chemokine receptor 3 (CCR3) gene, promoter region
 DEFINITION and partial sequence.
 ACCESSION AF247359
 VERSION AF247359.1 GI:19110540
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1454)
 AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and Michael,N.L.
 TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence for a Rare TATA-less Promoter Structure Conserved between Drosophila and Humans
 JOURNAL Genomics 80 (1), 86-95 (2002)
 MEDLINE 22074933
 PUBMED 12079287
 REFERENCE 2 (bases 1 to 1454)
 AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
 TITLE Direct Submission
 JOURNAL Submitted (21-MAR-2000) Dept. of Mol. Diag. and Pathogenesis, U.S. Military HIV Research Program, 1600 E. Gude Drive, Rockville, MD 20850, USA
 FEATURES
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 /mol_type="genomic DNA"
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 /map="3p21; between CCR1 and CCR5"
 /clone="A7"
 /cell_type="peripheral blood mononuclear cell"
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 823..>1454
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ORIGIN
Query Match      100.0%; Score 22; DB 9; Length 1454;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTACCACTGGTCTCTCTGTGC 22
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Db 1083 GGTACCACTGGTCTCTCTGTGC 1104

RESULT 8
AX513212
LOCUS      AX513212
DEFINITION Sequence 11 from Patent WO02062848.
ACCESSION  AX513212
VERSION     AX513212.1 GI:23504275
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Rothenberg,M.E. and Zimmerman,N.
TITLE       Regulation of cc chemokine receptor 3 (ccr3) expression
JOURNAL     Patent: WO 02062848-A 11 15-AUG-2002;
CHILDREN'S HOSPITAL MEDICAL CENTER (US)
FEATURES    Location/Qualifiers
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Query Match      100.0%; Score 22; DB 6; Length 2895;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 1561 GGTACCACTGGTCTCTCTGTGC 1582

RESULT 9
AF237380S1
LOCUS      AF237380S1
DEFINITION Homo sapiens CCR3 gene, promoter and exon 1.
ACCESSION  AF237380
VERSION     AF237380.1 GI:10643652
SEGMENT     1 of 2
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Zimmerman,N., Daugherty,B.L., Kavanaugh,J.L., El-Awar,F.Y.,
Moulton,E.A. and Rothenberg,M.E.
TITLE       Analysis of the CC chemokine receptor 3 gene reveals a complex 5'
exon organization, a functional role for untranslated exon 1, and a
broadly active promoter with eosinophil-selective elements
JOURNAL     Blood 96 (7), 2346-2354 (2000)
MEDLINE     20458773
PUBMED      11001881
REFERENCE   2
AUTHORS     Daugherty,B.L.
TITLE       Direct Submission
JOURNAL     Submitted (22-FEB-2000) Immunology & Rheumatology, Merck Research
Laboratories, 126 East Lincoln Avenue, Rahway, NJ 07065, USA
LOCATION/Qualifiers
source      1..2895
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/chromosome="3"
/map="3p21"
/clone="350-38"
/clone_lib="BgIII fragment from phage p1 human genomic
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33..38
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1287..1292
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1552..1642
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/note="untranslated"
/number=1

promoter
CAAT_signal
CAAT_signal
exon

ORIGIN
Query Match      100.0%; Score 22; DB 9; Length 2895;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTACCACTGGTCTCTCTGTGC 22
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Db 1561 GGTACCACTGGTCTCTCTGTGC 1582

RESULT 10
AC138069
LOCUS      AC138069
DEFINITION Homo sapiens chromosome 3 clone RP13-546I2, complete sequence.
ACCESSION  AC138069
VERSION     AC138069.3 GI:28416170
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
Saenphimmachak,C., Buckley,D., Kibukawa,M., Raymond,C. and
Haugen,E.D.
TITLE       Direct Submission
JOURNAL     Unpublished
REFERENCE   2
AUTHORS     Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.
TITLE       Direct Submission
JOURNAL     Submitted (12-DEC-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
REFERENCE   3
AUTHORS     Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.
TITLE       Direct Submission
JOURNAL     Submitted (10-JAN-2003) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
REFERENCE   4
AUTHORS     Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
Saenphimmachak,C., Buckley,D., Kibukawa,M., Raymond,C. and
Haugen,E.D.
TITLE       Direct Submission
JOURNAL     Submitted (19-FEB-2003) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
COMMENT     On Feb 19, 2003 this sequence version replaced gi:27573398.
            ----- Genome Center
            Center: University of Washington Genome Center
            Center Code: UWGC
            Web site: http://www.genome.washington.edu
            Contact: uwgchgsu@u.washington.edu
            ----- Project Information
            Center project name: chr-3
            Center clone name: RP13-546I2 (bc0820)
            ----- Summary Statistics
            Sequencing vector: plasmid; 100% of reads

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Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 177210 bases at least Q40
 Consensus quality: 177313 bases at least Q30
 Consensus quality: 177334 bases at least Q20
 Insert size: 177334; sum-of-contigs
 Quality coverage: 9.3x in Q20 bases; sum-of-contigs

Overlapping Sequences:

5': RP11-793E15 (UWGC:bc0564) AC104439, 95469-bp overlap
 3': U95626, 42710-bp overlap

Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

HindIII

EcoRI

BglII

SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt
1239	1199	11125	10952	6306	6319
449	<800	2290	2310	2067	2071
510	<800	560	<800	3913	3756
6511	6363	54	<800	2169	2210
5296	5509	1159	1158	910	910
10424	10027	4052	4034	875	883
5046	5119	1846	1829	3716	3756
1196	1199	8334	8273	4502	4523
1397	1392	12882	12573	1967	1945
2597	2624	448	<800	2864	2871
1688	1674	12737	12573	4724	4738
3800	3818	10300	10103	4773	4738
2248	2269	6671	6656	3707	3756

1055	4052	4034	336	<800
7718	1392	1386	79	<800
959	4253	4286	4736	4738
<800	2791	2834	1889	1945
1055	2647	2682	3696	3756
5759	3423	3409	1569	1539
5363	73	<800	8078	8038
3093	499	<800	1365	1325
959	723	<800	289	<800
4244	2763	2834	11047	10790
4857	6594	6656	8848	8963
3818	4503	4468	1914	1945
7718	5154	5136	1336	1325
3818	4730	4713	11485	11341
2376	13628	13324	974	975
868	166	<800	2448	2501
1674	9554	9494	373	<800
5759	1398	1386	1003	975
3818	1613	1641	1787	1756
1854	1479	1503	857	893
7718	1540	1503	1974	1945
1155	520	<800	1707	1631
7139	219	<800	3835	3756
2868	1571	1503	6586	6551
<800	154	<800	178	<800
1055	5077	5136	2905	2871
<800	2156	2190	2500	2501
6864	1075	1089	389	<800
<800	162	<800	41	<800
2749	2752	2834	685	<800
3416	1647	1641	2598	2662
3238	7059	7056	248	<800
5759	1547	1503	2152	2210
1497	5163	5136	431	<800
1392	8679	8719	237	<800
8333	2033	2035	3380	3411
6614	886	892	5694	5744

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645 <800 3265
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1026 1055 <800
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14333 14484 3144
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10701 10790
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Best Local Similarity 100.0%; Pred. No. 0.0094; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACCACCTGGTCTTCTTGTGC 22
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Db 65693 GGTACCACCTGGTCTTCTTGTGC 65714

RESULT 11
AC104439
LOCUS AC104439 197279 bp DNA linear PRI 20-JUN-2002
DEFINITION Homo sapiens chromosome 3 clone RP11-793E15, complete sequence.
ACCESSION AC104439 AC024739
VERSION AC104439.2 GI:21490240
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 197279)
AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
Saenphimmachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond,C.
and Haugen,E.D.
Direct Submission
Unpublished
2 (bases 1 to 197279)
AUTHORS Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.
Direct Submission
Submitted (11-DEC-2001) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
3 (bases 1 to 197279)
AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
Saenphimmachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond,C.
and Haugen,E.D.
Direct Submission
Submitted (20-JUN-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
On Jun 20, 2002 this sequence version replaced gi:17488621.
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Center: University of Washington Genome Center
Center Code: UWGC
Web site: http://www.genome.washington.edu
Contact: uwgctgsen.washington.edu
Drafting Center: WUGSC
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Project Information
Center project name: chr-3
Center clone name: RP11-793E15 (bc0564)
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Summary Statistics
Sequencing vector: unknown; 52% of reads
Sequencing vector: plasmid; L08752; 48% of reads
Chemistry: Dye-terminator ET; 94% of reads
Chemistry: Dye-terminator Big Dye; 6% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 197168 bases at least Q40
Consensus quality: 197255 bases at least Q30
Consensus quality: 197275 bases at least Q20
Insert size: 197279; sum-of-contigs
Quality coverage: 8.2x in Q20 bases; sum-of-contigs
Overlapping Sequences:

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5': RP11-91E8 (UWGC:bc0216) AC026349
3': CTD-2563A18 (UWGC:bc0730)

Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality zero.

Quality levels above 40 are expected to have less than

1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the

Genbank flat file format but are available as part

of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:
all regions were either double-stranded or sequenced with an
alternate chemistry or covered by high quality data (i.e., Phred
quality >= 30); an attempt was made to resolve all sequencing
problems, such as compressions and repeats; all regions were
covered by at least one plasmid subclone or more than one M13
subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest
fingerprinting. Comparison of the experimentally derived digest
fragments with sequence-predicted fragments is given below.
The electronically-digested sequence consists of both insert and
vector, in order to accurately represent the entire circular BAC.
Small fragments below a variable cutoff (approximately 400-800 bp)
are not resolved in the fingerprint and hence do not appear
in the table. There are no significant remaining discrepancies
between the experimental and predicted values. Uniquely ordered
fragments are separated by dashed lines.

HindIII

SeqDerMap	FrgrPrnt	SeqDerMap	FrgrPrnt	SeqDerMap	FrgrPrnt
2687	2617	8949	8586	8696	8661
6382	6410	2067	2160	6	<800
512	<800	7846	7940	2742	2803
449	<800	3734	3895	5376	5324
2602	2763	1334	1301	1493	1478
2590	2617	2287	2309	823	835
8313	8291	1814	1918	1962	2002
1711	1683	691	<800	2900	2954
9821	9472	5477	5348	1484	1478
516	<800	305	<800	1005	995
5587	8291	25245	25541	1181	1171
7446	7581	3988	4121	18560	19002
2088	2075	1633	1598	3603	3579
2509	2617	631	<800	4943	5076
3519	3501	90	<800	3239	3241
26	<800	402	<800	953	995
925	933	3350	3490	1621	1615
98	<800	4577	4515	6827	6900

Overlapping Sequences:

6409	6410	1229	1183	79	<800
1383	1376	4221	4331	16418	16263
16048	15829	3980	4121	3361	3241
1876	1877	2548	2497	872	881
4169	4068	674	<800	4220	4193
1674	1683	2332	2309	2848	2803
52	<800	11445	11045	2283	2318
5227	5082	5692	5632	3211	3241
15464	15829	1385	1414	4615	4632
14333	14296	608	<800	6823	6900
1026	1026	3930	3895	886	881
645	<800	1465	1414	2032	2002
6621	6410	2382	2497	8680	8661
8413	8291	747	<800	5163	5076
1401	1376	1951	2012	1547	1478
1512	1471	642	<800	7058	6900
5801	5644	21060	21003	1647	1615
3256	3278	3700	3666	2753	2803
3448	3501	1321	1301	162	<800
2738	2763	10705	10502	1078	1093
237	<800	3128	3317	2156	2173
6715	6823	183	<800	5077	5076
201	<800	3255	3490	154	<800
1002	1026	5693	5632	1571	1478
221	<800	3380	3317	219	<800
2854	2899	237	<800	520	<800
6998	7317	431	<800	1540	1478
1174	1145	2152	2160	1479	1478
7876	8291	249	<800	1613	1615
1911	1877	2599	2778	1399	1478
3899	3847	685	<800	9553	9383
5672	5644	41	<800	166	<800
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Query Match 100.0%; Score 22; DB 9; Length 197279;
 Best Local Similarity 100.0%; Pred. No. 0.0093;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTACCACTGGTCTTCTTGTC 22
 Db 167486 GGTACCACTGGTCTTCTTGTC 167507

RESULT 12
 LOCUS HSA312688

DEFINITION HSA312688 220965 bp DNA linear HTG 15-MAY-2002
 Homo sapiens chromosome 3 clone RP6-32g23 map 3p21.3, ***
 SEQUENCING IN PROGRESS ***, 26 ordered pieces.

ACCESSION AJ312688.2 GI:13559235

VERSION HTG; HTGS PHASE2.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Kiss,H.; Yang,X.; Kiss,C.; Andersson,X.; Klein,G.; Imreh,S. and

Dumanski,J.P.

TITLE The transcriptional map of the common eliminated region 1 (C3CER1)

JOURNAL in 3p21.3

MEDLINE Eur. J. Hum. Genet. 10 (1), 52-61 (2002)

PUBMED 21906202

REFERENCE 2 (bases 1 to 220965)

AUTHORS Kiss,H.

TITLE Direct Submission

JOURNAL Submitted (01-APR-2001) Kiss H., Microbiology and Tumorbiology

Center (MTC), Karolinska Institute, Box 280, Stockholm, S-17177,

SWEDEN

COMMENT On Apr 5, 2001 this sequence version replaced gi:13548633.

The sequence is a consensus sequence of clone RP4-787c23 (1-140400

bp),

clone RP6-32g23 (31212-220965 bp), clone RP6-146e1 (partially,

1-6800 bp)

and clone RP6-188g11 (partially, 1-108303 bp). The sequencing

contigs are

in order and the gaps between them are represented by 100 Ns.

Contig 1:

1-11731 bp Contig 2: 11832-26218 bp Contig 3: 26319-28347 bp

Contig 4:

28448-42160 bp Contig 5: 42261-55059 bp Contig 6: 55160-61578 bp

Contig 7: 61679-97342 bp Contig 8: 97443-117655 bp Contig 9:

117756-118727 bp

Contig 10: 118828-121834 bp Contig 11: 121935-127855 bp Contig

12:

127956-129383 bp Contig 13: 129484-131747 bp Contig 14:

131848-132316 bp

Contig 15: 132417-134455 bp Contig 16: 134556-135527 bp Contig

17:

135628-189051 bp Contig 18: 189152-189476 bp Contig 19:

189577-191375 bp

Contig 20: 191476-201473 bp Contig 21: 201574-202307 bp Contig

22:

202408-204878 bp Contig 23: 204979-213531 bp Contig 24:

213632-218109 bp

Contig 25: 218210-219800 bp Contig 26: 219901-220965 bp.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 26 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submitter.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
 * 1 11731: contig of 11731 bp in length
 * 11732 11831: gap of 100 bp
 * 11832 26218: contig of 14387 bp in length
 * 26219 26318: gap of 100 bp
 * 26319 28347: contig of 2029 bp in length
 * 28348 28447: gap of 100 bp
 * 28448 42160: contig of 13713 bp in length
 * 42161 42360: gap of 200 bp
 * 42361 55059: contig of 12699 bp in length
 * 55060 55159: gap of 100 bp
 * 55160 61578: contig of 6419 bp in length
 * 61579 61678: gap of 100 bp
 * 61679 97342: contig of 35664 bp in length
 * 97343 97442: gap of 100 bp
 * 97443 117655: contig of 20213 bp in length
 * 117656 117755: gap of 100 bp
 * 117756 118727: contig of 972 bp in length
 * 118728 118827: gap of 100 bp
 * 118828 121834: contig of 3007 bp in length
 * 121835 121934: gap of 100 bp
 * 121935 127855: contig of 5921 bp in length
 * 127856 127955: gap of 100 bp
 * 127956 129383: contig of 1428 bp in length
 * 129384 129483: gap of 100 bp
 * 129484 131747: contig of 2264 bp in length
 * 131748 132316: contig of 469 bp in length
 * 132317 132416: gap of 100 bp
 * 132417 134455: contig of 2039 bp in length
 * 134456 134556: gap of 100 bp
 * 134557 135527: contig of 972 bp in length
 * 135528 135627: gap of 100 bp
 * 135628 189051: contig of 53424 bp in length
 * 189052 189151: gap of 100 bp
 * 189152 189476: contig of 325 bp in length
 * 189477 189576: gap of 100 bp
 * 189577 191375: contig of 1799 bp in length
 * 191376 191475: gap of 100 bp
 * 191476 201473: contig of 9998 bp in length
 * 201474 201573: gap of 100 bp
 * 201574 202307: contig of 734 bp in length
 * 202308 202407: gap of 100 bp
 * 202408 204878: contig of 2471 bp in length
 * 204879 204979: gap of 100 bp
 * 204980 213531: contig of 8553 bp in length
 * 213532 213631: gap of 100 bp
 * 213632 218109: contig of 4478 bp in length
 * 218110 218209: gap of 100 bp
 * 218210 219800: contig of 1591 bp in length
 * 219801 219900: gap of 100 bp
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Db 121110 GGTACCACTGGTCTCTTTGTGC 121131

RESULT 13
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 Sequence 22 from Patent WO02062848.
 AX513223
 ACCESSION
 VERSION
 AX513223.1 GI:23504286
 KEYWORDS
 Homo sapiens (human)
 SOURCE
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1
 Rothenberg M.E. and Zimmerman N.
 Regulation of cc chemokine receptor 3 (ccr3) expression
 Patent: WO 02062848-A 22 15-AUG-2002;
 CHILDREN'S HOSPITAL MEDICAL CENTER (US)
 FEATURES
 Location/Qualifiers
 1. .21
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 /mol_type="unassigned RNA"
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 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTACCACTGGTCTCTTTGTG 21

Db 1 GGTACCACTGGTCTCTTTGTG 21

RESULT 14

AF224495
 LOCUS
 DEFINITION
 Homo sapiens CC chemokine receptor 3 (CCR3) mRNA, partial cds.
 AF224495
 ACCESSION
 VERSION
 AF224495.1 GI:13924481
 KEYWORDS
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (Bases 1 to 260)
 Scotet, E.J.
 CCR3 expression is associated with chromatin remodeling in Th2
 cells
 JOURNAL
 Unpublished
 REFERENCE
 2 (bases 1 to 260)
 Scotet, E.J.
 AUTHORS
 Direct Submission
 TITLE
 Submitted (13-JAN-2000) Basel Institute for Immunology, 487
 Grenzacherstrasse, Basel CH-4005, Switzerland
 JOURNAL
 Location/Qualifiers
 1. .260
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 /db_xref="GI:13924482"
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FEATURES

source

gene

CDS

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS AF262301 406 bp mRNA linear PRI 26-JUN-2002
DEFINITION Homo sapiens clone 4 CC chemokine receptor 3 (CCR3) mRNA, partial
cds.
ACCESSION AF262301
VERSION AF262301.1 GI:19171644
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 406)
Vijh,S., Dayhoff,D.E., Wang,C.E., Inam,Z., Ehrenberg,P.K. and
Michael,N.L.
REFERENCE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence
AUTHORS for a Rare TATA-Less Promoter Structure Conserved between
Drosophila and Humans
JOURNAL Genomics 80 (1), 86-95 (2002)
MEDLINE 22074933
PubMed 12079287
REFERENCE 2 (bases 1 to 406)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
TITLE Direct Submission
JOURNAL Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis,
Walter Reed Army Institute of Research, 1600 E. Gude Drive,
Rockville, MD 20850, USA
FEATURES
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location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="3"
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/gene="CCR3"
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/codon_start=1
/product="CC chemokine receptor 3"
/protein_id="AA185630.1"
/db_xref="GI:19171645"
/translation="MTTSLDTVETFGTISVYDDVGLLCEKADTRALMAQFVPPPLYSIV
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Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ACCACTGGTCTCTTTGTGC 19

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Job time : 494.914 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Title: US-10-068-067-17

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Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	15	68.2	118067	US-08-497-855A-32	Sequence 32, Appl
3	14	63.6	495	US-09-621-976-17953	Sequence 17953, A
4	14	63.6	508	US-09-621-976-9046	Sequence 9046, Ap
5	14	63.6	542	US-09-669-751-135	Sequence 135, App
6	14	63.6	698	US-09-634-238-126	Sequence 126, Appl
7	14	63.6	865	US-09-640-419C-6	Sequence 6, Appli
8	14	63.6	1760	US-09-495-050A-139	Sequence 139, App
9	14	63.6	2114	US-08-370-838-158	Sequence 158, App
10	14	63.6	3142	US-08-110-158-3	Sequence 3, Appli
11	14	63.6	3142	US-09-023-655-1090	Sequence 1090, Ap
12	14	63.6	3144	PCT-US91-05059-1	Sequence 1, Appli
13	14	63.6	3812	US-08-188-582-19	Sequence 19, Appl
14	14	63.6	3812	US-08-646-715-19	Sequence 19, Appl
15	13	59.1	21	US-09-422-978-9067	Sequence 9067, Ap
16	13	59.1	285	US-08-333-294A-1150	Sequence 1150, Ap
17	13	59.1	698	US-08-998-416-756	Sequence 756, App
18	13	59.1	882	US-09-543-681A-1777	Sequence 1777, Ap
19	13	59.1	914	US-09-673-395A-114	Sequence 114, App
20	13	59.1	1104	US-09-252-991A-13171	Sequence 13171, A
21	13	59.1	1152	US-09-461-325-38	Sequence 38, Appl
22	13	59.1	1152	US-10-012-542-38	Sequence 38, Appl
23	13	59.1	1301	US-08-489-847-108	Sequence 108, App
24	13	59.1	1308	US-09-205-258-215	Sequence 215, App
25	13	59.1	1457	US-09-673-395A-554	Sequence 554, App
26	13	59.1	1457	US-09-673-395A-554	Sequence 554, App
27	13	59.1	1471	US-09-620-312D-446	Sequence 446, App

Sequence 3779, Ap
Sequence 12780, A
Sequence 11, Appl
Sequence 8, Appl
Sequence 6, Appl
Sequence 20, Appl
Sequence 800, App
Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 48, Appl
Sequence 1298, Ap
Sequence 18, Appl
Sequence 22, Appl
Sequence 37, Appl
Sequence 3185, Ap
Sequence 11, Appl
Sequence 2, Appl
Sequence 2, Appl

US-09-328-352-3779
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US-09-782-906-6
US-09-620-312D-800
US-08-420-235B-20
US-08-793-624-20
PCT-US95-10194-20
US-09-205-258-48
US-09-489-039A-1298
US-09-445-041-18
US-09-078-972A-22
US-09-282-147-37
US-09-134-000C-3185
US-10-164-595-11
US-09-248-571-2
US-09-553-736-2

ALIGNMENTS

RESULT 1
US-09-134-513-1
; Sequence 1, Application US/09134513
; Patent No. 6210964
; GENERAL INFORMATION:
; APPLICANT: Brown, Edward M.
; APPLICANT: Diaz, Ruben
; APPLICANT: Bai, Mei
; APPLICANT: Quinn, Stephen J.
; TITLE OF INVENTION: The Avian Extracellular Calcium-Sensing
; TITLE OF INVENTION: Receptor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Vinson & Elkins L.L.P.
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.
; ZIP: 20004-1008
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,513
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanzo, Michael A.
; REGISTRATION NUMBER: 36,912
; REFERENCE/DOCKET NUMBER: BR1331/13003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)639-6585
; TELEFAX: (202)639-6604
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
US-09-134-513-1

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Best Local Similarity 100.0%; Pred. No. 13;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 CTGGCTTCTTGTGC 22

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US-09-497-855A-32/c
; Sequence 32, Application US/09497855A
; Patent No. 6605432
; GENERAL INFORMATION:
; APPLICANT: Huang, Tim
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
; FILE REFERENCE: UMO1523
; CURRENT APPLICATION NUMBER: US/09/497,855A
; CURRENT FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/120,592
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 60/118,760
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 118067
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-497-855A-32

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Db      113196 TACCACTGGTCTTCT 113182
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RESULT 3
US-09-621-976-17953/c
; Sequence 17953, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 17953
; LENGTH: 495
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-621-976-17953

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 9046, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.

FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 9046
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-621-976-9046

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Best Local Similarity 100.0%; Pred. No. 49;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
US-09-669-751-135/c
; Sequence 135, Application US/09669751
; Patent No. 6551575
; GENERAL INFORMATION:
; APPLICANT: Greenspan, Ralph J.
; TITLE OF INVENTION: Methods for Identifying Compounds for
; TITLE OF INVENTION: Motion Sickness, Vertigo and Other Disorders Related to
; TITLE OF INVENTION: Balance and the Perception of Gravity
; FILE REFERENCE: P-NI 3864
; CURRENT APPLICATION NUMBER: US/09/669,751
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 60/168,579
; PRIOR FILING DATE: 1999-12-02
; NUMBER OF SEQ ID NOS: 261
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 135
; LENGTH: 542
; TYPE: DNA
; ORGANISM: Drosophila
; US-09-669-751-135

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6
US-09-634-238-126
; Sequence 126, Application US/09634238
; Patent No. 6544772
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Havukkala, Ilkka J.
; APPLICANT: Bloksberg, Leonard, N.
; APPLICANT: Lubbers, Mark W.
; APPLICANT: Dekker, James
; APPLICANT: Christenson, Anna C.
; APPLICANT: Holland, Ross
; APPLICANT: O'Toole, Paul W.
; APPLICANT: Reid, Julian R.
; APPLICANT: Coolbear, Timothy
; TITLE OF INVENTION: Polynucleotides, materials incorporating
; TITLE OF INVENTION: them and methods for using them.
; FILE REFERENCE: 11000.1043U1
; CURRENT APPLICATION NUMBER: US/09/634,238
; CURRENT FILING DATE: 2000-08-08
; NUMBER OF SEQ ID NOS: 422
; SOFTWARE: FastSEQ for Windows Version 4.0
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; SEQ ID NO 126
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; TYPE: DNA
; ORGANISM: Lactobacillus rhamnosus
; FEATURE:
; NAME/KEY: misc feature
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; OTHER INFORMATION: n = A,T,C or G
US-09-634-238-126

Query Match      63.6%; Score 14; DB 4; Length 698;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 7
US-09-640-419C-6/c
; Sequence 6, Application US/09640419C
; Patent No. 6830615
; GENERAL INFORMATION:
; APPLICANT: Bidney, Dennis L
; APPLICANT: Crasta, Oswald R
; APPLICANT: Hu, Xu
; APPLICANT: Lu, Guihua
; TITLE OF INVENTION: DEFENSE-RELATED SIGNALING GENES AND METHODS OF USE
; FILE REFERENCE: 35718/199009 (5718-92)
; CURRENT APPLICATION NUMBER: US/09/640.419C
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,656
; PRIOR FILING DATE: 1999-08-18
; PRIOR APPLICATION NUMBER: 60/206,405
; PRIOR FILING DATE: 2000-05-23
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 865
; TYPE: DNA
; ORGANISM: Helianthus annuus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(519)
US-09-640-419C-6

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Best Local Similarity 100.0%; Pred. No. 48;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 129 CTGGTCTCTCTGTG 116

RESULT 8
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; Sequence 139, Application US/09495050A
; Patent No. 6492505
; GENERAL INFORMATION:
; APPLICANT: Roopa, Reddy
; APPLICANT: Guegler, Karl, J.
; APPLICANT: Au-young, Janice
; TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED P
; FILE REFERENCE: PA-0013 US
; CURRENT APPLICATION NUMBER: US/09/495,050A
; CURRENT FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/118,318
; PRIOR FILING DATE: February 1, 1999
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: PERL Program
; SEQ ID NO 139
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; LENGTH: 1760
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6492505 1518320CT1
US-09-495-050A-139.

Query Match      63.6%; Score 14; DB 4; Length 1760;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CTGGTCTCTCTGTG 21
Db 1432 CTGGTCTCTCTGTG 1419

RESULT 9
US-09-370-838-158
; Sequence 158, Application US/09370838
; Patent No. 6444425
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Roadoh
; APPLICANT: Secret, Heather
; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
; FILE REFERENCE: 210121.475C1
; CURRENT APPLICATION NUMBER: US/09/370,838
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: US 09/285,323
; EARLIER FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 289
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 158
; LENGTH: 2114
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-370-838-158

Query Match      63.6%; Score 14; DB 4; Length 2114;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTACCACCTGGTCT 14
Db 1463 GGTACCACCTGGTCT 1476

RESULT 10
US-08-110-158-3/c
; Sequence 3, Application US/08110158
; Patent No. 5605821
; GENERAL INFORMATION:
; APPLICANT: McEver, Rodger P.
; APPLICANT: Pan, Junliang
; TITLE OF INVENTION: Expression Control Sequences of the
; TITLE OF INVENTION: P-Selectin Gene
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/08/110,158
FILING DATE: 19930820
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/320,408
FILING DATE: 08-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
TELEPHONE: (404)-815-6508
TELEFAX: (404)-815-6555
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3142 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: linear
CDNA

Query Match 63.6%; Score 14; DB 1; Length 3142;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CTGGTCTTCTTG 21
|||||
Db 2822 CTGGTCTTCTTG 2809

RESULT 11
US-09-023-655-1090/c
Sequence 1090, Application US/09023655
Patent No 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhammer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1090:
LENGTH: 3142 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: G183390
US-09-023-655-1090
Query Match 63.6%; Score 14; DB 4; Length 3142;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CTGGTCTTCTTG 21
|||||
Db 2822 CTGGTCTTCTTG 2809

RESULT 12
PCT-US91-05059-1/c
Sequence 1, Application PC/TUS9105059
GENERAL INFORMATION:
APPLICANT: Regents of the Board of the, University of
APPLICANT: Oklahoma
TITLE OF INVENTION: Functionally Active Selectin-Derived
Peptides
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick & Cody
STREET: 100 Peachtree Street, Suite 3100
CITY: Atlanta
STATE: Georgia
COUNTRY: US
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05059
FILING DATE: 19910717
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/320408
FILING DATE: 08-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554199
FILING DATE: 17-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF110CIP
TELEPHONE: 404-572-6508
TELEFAX: 404-572-6555
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3144 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: YES
ANTI-SENSE: YES
PRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapien
TISSUE TYPE: Blood
CELL TYPE: Endothelial
FEATURE:
NAME/KEY: polyA signal
LOCATION: 2833-2838
OTHER INFORMATION: /note= "Potential polyadenylation
OTHER INFORMATION: signals"
FEATURE:

; NAME/KEY: polya signal
; LOCATION: 3124..3130
; OTHER INFORMATION: /note="Potential polyadenylation
; OTHER INFORMATION: signal"
PCT-US91-05059-1

Query Match 63.6%; Score 14; DB 5; Length 3144;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACTGGTCTCTTG 21
|||||

Db 2822 CTGGTCTCTCTTG 2809
|||||

RESULT 13

US-08-189-582-19/c
; Sequence 19, Application US/08189582
; Patent No. 5534410
; GENERAL INFORMATION:
; APPLICANT: Tjian, Robert
; APPLICANT: Comai, Lucio
; APPLICANT: Dynlacht, Brian D.
; APPLICANT: Hoey, Timothy
; APPLICANT: Ruppert, Siegfried
; APPLICANT: Tanese, Naoko
; APPLICANT: Wang, Edith
; APPLICANT: Weinzierl, Robert O.J.
; TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFs AND METHODS OF USE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/189,582
; FILING DATE: 28-JAN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3812 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 60..3701
US-08-189-582-19

Query Match 63.6%; Score 14; DB 1; Length 3812;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CACTGGTCTCTTG 19
|||||

Db 3126 CACTGGTCTCTTG 3113

RESULT 14

US-08-646-715-19/c
; Sequence 19, Application US/08646715
; Patent No. 5637686
; GENERAL INFORMATION:
; APPLICANT: Tjian, Robert
; APPLICANT: Comai, Lucio
; APPLICANT: Dynlacht, Brian D.
; APPLICANT: Hoey, Timothy
; APPLICANT: Ruppert, Siegfried
; APPLICANT: Tanese, Naoko
; APPLICANT: Wang, Edith
; APPLICANT: Weinzierl, Robert O.J.
; TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFs AND METHODS OF USE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,715
; FILING DATE: 09-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/188,582
; FILING DATE: 28-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3812 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 60..3701
US-08-646-715-19

Query Match 63.6%; Score 14; DB 1; Length 3812;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CACTGGTCTCTTG 19
|||||

Db 3126 CACTGGTCTCTTG 3113

RESULT 15

US-09-422-978-9067
; Sequence 9067, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel

; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 9067
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..21
; OTHER INFORMATION: downstream amplification primer 99-2170 for SEQ 1202, in compleme
US-09-422-978-9067

Query Match 59.1%; Score 13; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GGTCCTCTTGTGC 22
|||||
Db 1 GGTCCTCTTGTGC 13

Search completed: August 2, 2004, 20:30:03
Job time : 23.1897 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 18:06:45 ; Search time 909.207 Seconds

(without alignments)

722.573 Million cell updates/sec

Title: US-10-068-067-17

Perfect score: 22

Sequence: 1 ggtaccactgctctcttctgtgc 22

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

1: em_estba.*

2: em_esthum.*

3: em_estin.*

4: em_estm.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_htc.*

9: gb_est1.*

10: gb_est2.*

11: gb_hcc.*

12: gb_est3.*

13: gb_est4.*

14: gb_est5.*

15: em_estfun.*

16: em_estom.*

17: em_gss_hum.*

18: em_gss_inv.*

19: em_gss_pln.*

20: em_gss_vrt.*

21: em_gss_fun.*

22: em_gss_mam.*

23: em_gss_mus.*

24: em_gss_pro.*

25: em_gss_rod.*

26: em_gss_phg.*

27: em_gss_vrl.*

28: gb_gss1.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	17	77.3	613	28	BH299085
C 2	17	77.3	905	10	BF340232
C 3	16	72.7	221	10	BF557219
C 4	16	72.7	224	9	AA957733

C 5	16	72.7	322	10	AW826871
C 6	16	72.7	346	12	BG738607
C 7	16	72.7	364	10	BF389025
C 8	16	72.7	406	9	AI112888
C 9	16	72.7	422	13	EX307267
C 10	16	72.7	433	14	CB495381
C 11	16	72.7	433	14	CB495414
C 12	16	72.7	433	14	CB495567
C 13	16	72.7	451	13	BY505647
C 14	16	72.7	456	10	BF388753
C 15	16	72.7	500	10	BF402543
C 16	16	72.7	522	10	BE831025
C 17	16	72.7	552	12	BJ057835
C 18	16	72.7	569	29	CE396889
C 19	16	72.7	601	14	CB495211
C 20	16	72.7	624	28	AQ744376
C 21	16	72.7	674	12	BI296051
C 22	16	72.7	677	14	CB499837
C 23	16	72.7	700	29	AG138506
C 24	16	72.7	723	9	AU056819
C 25	16	72.7	742	29	AG059138
C 26	16	72.7	744	29	CG957943
C 27	16	72.7	766	29	CG675256
C 28	16	72.7	797	28	BZ122800
C 29	16	72.7	832	10	BF248442
C 30	16	72.7	838	14	CK017521
C 31	16	72.7	846	28	BZ215165
C 32	16	72.7	882	10	BF300865
C 33	16	72.7	918	29	CNS051G8
C 34	16	72.7	944	29	CNS04H92
C 35	16	72.7	1053	28	CC283410
C 36	16	72.7	1117	12	BG829094
C 37	15	68.2	121	12	BQ034576
C 38	15	68.2	172	14	CK104844
C 39	15	68.2	174	12	BI005360
C 40	15	68.2	201	29	AL755014
C 41	15	68.2	297	10	BE523740
C 42	15	68.2	319	13	BY151693
C 43	15	68.2	330	13	EX635885
C 44	15	68.2	342	12	EM386785
C 45	15	68.2	359	10	BE688637

ALIGNMENTS

RESULT 1
BH299085/c

LOCUS

DEFINITION

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BH299085 613 bp DNA linear GSS 30-NOV-2001
CH230-146H22.TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone
CH230-146H22, genomic survey sequence.

BH299085
GSS.

BH299085.1 GI:17211493
Rattus norvegicus (Norway rat)

Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus
1 (bases 1 to 613)

Zhao,S., Shetty,J., Shatsman,S., Tsengye,G., Geer,K.,
Shvartsbeyn,A., Gebregorgis,E., Overton,L., Russell,D., Chen,D.,
Riggs,F., de Jong,P. and Fraser,C.M.

Rat BAC End Sequences from Library CHORI-230 EcoRI segment
Unpublished (1999)

Other GSSs: CH230-146H22.TV
Contact: Shaying Zhao

Department of Eukaryotic Genomics
The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200

Fax: 301 838 0208
Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230
(<http://www.chori.org/bacpac/rat230.htm>). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.choi.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or_xing_information.htm). BAC end
plate: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 146 row: H column: 22
Seq primer: SP6
Class: BAC ends.

FEATURES

Location/Qualifiers

source

1. .613
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-146H22"
/sex="female"
/cell_type="Brain"
/clone_lib="CHORI-230 Segment 1"
/notes="Vector: PTABAC2.1; Site 1: EcoRI; Site 2: EcoRI;
CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
Pieter de Jong"

ORIGIN

Query Match 77.3%; Score 17; DB 28; Length 613;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACTGGTCTCTCTGTG 21

Db 172 CCACTGGTCTCTCTGTG 156

RESULT 2

BF340232/c 905 bp mRNA linear EST 22-NOV-2000
LOCUS 602036821F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4184908
DEFINITION 5', mRNA sequence.

ACCESSION BF340232

VERSION BF340232.1 GI:11286694

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 905)

TITLE NIH-MGC <http://mgs.nci.nih.gov/>.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: David N. Louis, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LHAM9503 row: i column: 05

High quality sequence stop: 675.

FEATURES

Location/Qualifiers

source

1. .905
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4184908"
/tissue_type="glioblastoma with EGFR amplification"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP Brn64"
/notes="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI. Cloned unidirectionally. Primer: oligo dt.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

ORIGIN

Query Match 77.3%; Score 17; DB 10; Length 905;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ACCACTGGTCTCTCTGT 20

Db 674 ACCACTGGTCTCTCTGT 658

RESULT 3

BF557219

LOCUS

BF557219 221 bp mRNA linear EST 12-DEC-2000
DEFINITION UI-R-E1-gc-b-11-0-UI-r1 UI-R-E1 Rattus norvegicus cDNA clone
UI-R-E1-gc-b-11-0-UI 5', mRNA sequence.

ACCESSION BF557219

VERSION BF557219.1 GI:11666949

KEYWORDS EST.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM

Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 221)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene
discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 889548

COMMENT

Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road, 4156 MEBRP, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

CDNA Library Preparation: M.B. Soares Lab Clone distribution:

clones will be available through Research Genetics (www.resgen.com)

This clone is also available through the I.M.A.G.E. Consortium at

LLNL (info@image.llnl.gov). IMAGE ID= 1772378

Seq primer: M13 Forward.

Location/Qualifiers

source

1. .221
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-E1-gc-b-11-0-UI"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="UI-R-E1"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-E1
library is a subtracted library derived from the UI-R-E0
library. The UI-R-E0 library consisted of a mixture of
individually tagged normalized libraries constructed from
8, 12 and 18-day embryo. The tag is a string of 3-5
nucleotides present between the Not I site and the
oligo-dt track which allows identification of the library
of origin of a clone within the mixture. The subtracted
library (UI-R-E1) was constructed as follows: PCR
amplified cDNA inserts from a pool of UI-R-E0 clones from
which 3' ESTs had been derived was used as a driver in a
hybridization with the UI-R-E0 library in the form of
circles (subtracted library). The remaining single-stranded
hydroxyapatite column chromatography, converted to
double-stranded circles and electroporated into DH10B
bacteria (Life Technologies) to generate the UI-R-E1
library. This procedure has been previously described
(Bonaldo, Lennon and Soares, Genome Research 6: 791-806,

1996")

ORIGIN

Query Match 72.7%; Score 16; DB 10; Length 221;
 Best Local Similarity 100.0%; Pred. No. 6.5e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CACTGGTCTTCTGTG 21

Db 93 CACTGGTCTTCTGTG 108

RESULT 4

AA957733/c
 LOCUS 224 bp mRNA linear EST 04-JUL-1999
 DEFINITION UI-R-E1-gc-b-11-0-UI.s1 UI-R-E1 Rattus norvegicus cDNA clone
 UI-R-E1-gc-b-11-0-UI 3', mRNA sequence.

ACCESSION AA957733

VERSION AA957733.1 GI:4277623

KEYWORDS EST.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE 1 (bases 1 to 224)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene
 discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 9704477

PubMed 889548

COMMENT On May 7, 1998 this sequence version replaced gi:3121428.

Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

The sequence tag present in the cDNA between the NotI site and the
 oligo-dT track served to identify it as a clone from the normalized
 adult 18-day-embryo library. cDNA Library Preparation: M. Fatima
 Bonaldo, Ph.D. Clone distribution: clones will be available through
 Research Genetics. This clone is also available through the
 I.M.A.G.E. Consortium at LLNL (info@image.llnl.gov). IMAGE

ID=1772378

Seq primer: M13 Forward

POLYA=No.

FEATURES

source

1. .224
 Location/Qualifiers
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-E1-gc-b-11-0-UI"
 /dev_stage="adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="UI-R-E1"
 /note="Vector: pMT73D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-E1
 library is a subtracted library derived from the UI-R-E0
 library. The UI-R-E0 library consisted of a mixture of
 individually tagged normalized libraries constructed from
 8, 12 and 18-day embryo. The tag is a string of 3-5
 nucleotides present between the Not I site and the
 oligo-dT track which allows identification of the library
 of origin of a clone within the mixture. The subtracted
 library (UI-R-E1) was constructed as follows: PCR
 amplified cDNA inserts from a pool of UI-R-E0 clones from
 which 3' ESTs had been derived was used as a driver in a
 hybridization with the UI-R-E0 library in the form of
 single-stranded circles. The remaining single-stranded

circles (subtracted library) was purified by
 hydroxyapatite column chromatography, converted to
 double-stranded circles and electroporated into DH10B
 bacteria (Life Technologies) to generate the UI-R-E1
 library. This procedure has been previously described
 (Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
 1996)"

ORIGIN

Query Match 72.7%; Score 16; DB 9; Length 224;
 Best Local Similarity 100.0%; Pred. No. 6.5e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CACTGGTCTTCTGTG 21

Db 129 CACTGGTCTTCTGTG 114

RESULT 5

AW826871/c
 LOCUS 322 bp mRNA linear EST 13-FEB-2002
 DEFINITION fx54a12.y1 zebrafish adult retina cDNA Danio rerio CDNA 5' similar
 to TR:042104 042104 ARRESTIN. ;, mRNA sequence.

ACCESSION AW826871

VERSION AW826871.1 GI:7919948

KEYWORDS EST.

SOURCE Danio rerio (zebrafish)

ORGANISM

Danio rerio
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.

REFERENCE 1 (bases 1 to 322)

AUTHORS

Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
 Bady,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
 Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
 Persson,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
 Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
 Waterston,R. and Wilson,R.
 WashU Zebrafish EST Project 1998

TITLE

JOURNAL

COMMENT

Contact: Stephen L. Johnson
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: zbzfsh@watson.wustl.edu

Library constructed by: Chandra Tucker and Gregory Niemi DNA
 Sequencing by: Washington University Genome Sequencing Center Clone
 distribution: RessourcenzentrumPrimatDatenbank, Berlin, Germany
 (web address: www.rzpd.de)

Trace considered overall poor quality

Seq primer: T3 ET from Amersham

High quality sequence stop: 1.

FEATURES

source

1. .322
 Location/Qualifiers
 /organism="Danio rerio"
 /mol_type="mRNA"
 /strain="wild-type"
 /db_xref="taxon:7955"
 /sex="mixed"
 /dev_stage="1-2 years"
 /lab_host="E.Coli XL1-Blue MRF" (XLI-Blue MRF)"
 /clone_lib="Zebrafish adult retina cDNA"
 /note="Vector: Lambda ZAP II (phagescript SK-); Site 1:
 EcoRI; Site 2: SalI; This Zebrafish library was
 constructed by Dr. Susan B. Brockerhoff (email:
 sbrockers@u.washington.edu) RZPD library number: 760"

ORIGIN

Query Match 72.7%; Score 16; DB 10; Length 322;
 Best Local Similarity 100.0%; Pred. No. 6.6e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACTGGTCTTCTGT 20
 |||||
 Db 30 CCACTGGTCTTCTGT 15

RESULT 6

LOCUS

BF38607/c
 DEFINITION
 IP60f09.y1 Zebrafish adult retina cDNA Danio rerio cDNA clone
 IMAGE:4786337 5' similar to TR:042104 042104 ARRESTIN. ;, mRNA
 sequence.

ACCESSION

BF38607
 VERSION
 KEYWORDS

SOURCE

Danio rerio (zebrafish)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.

REFERENCE

1 (bases 1 to 346)
 Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
 Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wyllie,T.,
 Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
 Persson,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
 Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
 Waterston,R. and Wilson,R.
 WashU Zebrafish EST Project 1998

TITLE

JOURNAL

COMMENT

Unpublished (1998)
 Contact: Stephen L. Johnson
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: zbrafish@wustl.edu

Library constructed by: Chandra Tucker and Gregory Niemi DNA
 Sequencing by: Washington University Genome Sequencing Center Clone
 distribution: Ressourcenzentrum/PrimarDatenbank, Berlin, Germany
 (web address: www.rzpd.de)

Trace considered overall poor quality

Seq primer: T3 ET from Amersham

High quality sequence stop: 1.

FEATURES

source

1. 346
 Location/Qualifiers
 /organism="Danio rerio"
 /mol_type="mRNA"
 /strain="wild-type"
 /db_xref="taxon:7955"
 /clone="IMAGE:4786337"
 /sex="mixed"
 /dev_stage="1-2 years"
 /lab_host="E.Coli XL1-Blue MRF' (XL1-Blue MRF')"
 /clone_lib="Zebrafish adult retina cDNA"
 /notes="Vector: Lambda ZAP II (pBluescript SK-); Site_1:
 EcoRI; Site_2: SalI; This Zebrafish library was
 constructed by Dr. Susan B. Brockerhoff (email:
 sbrocker@u.washington.edu) RZPD library number: 760"

ORIGIN

Query Match 72.7%; Score 16; DB 12; Length 346;
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;
 Mismatches 0; Gaps 0; Indels 0; Gaps 0;

QY 5 CCACTGGTCTTCTGT 20
 |||||
 Db 24 CCACTGGTCTTCTGT 9

RESULT 7

LOCUS

BF389025/c
 DEFINITION
 UI-R-BS2-bdk-h-10-0-UI.s1 UI-R-BS2 Rattus norvegicus cDNA clone
 UI-R-BS2-bdk-h-10-0-UI 3', mRNA sequence.

ACCESSION

BF389025

VERSION
 KEYWORDS
 SOURCE
 ORGANISM

BF389025.1 GI:11373852
 EST.
 Rattus norvegicus (Norway rat)
 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE

AUTHORS

1 (bases 1 to 364)
 Bonaldo,M.F., Lennon,G. and Soares,M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery

JOURNAL

MEDLINE

PUBMED

COMMENT

97044477
 8889548
 Contact: Soares, MB
 Coordinated Laboratory for Computational Genomics
 University of Iowa
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565

Email: bento-soares@uiowa.edu
 The sequence contained an oligo-dT track that was present in the
 oligonucleotide that was used to prime the synthesis of first
 strand cDNA and therefore this may represent a bonafide poly A
 tail. The sequence tag present in the cDNA between the NotI site
 and the oligo-dT track served to verify it as a clone from the
 normalized embryo at 13 dpc library cDNA Library Preparation: M.B.
 Soares Lab Clone distribution: clones will be available through
 Research Genetics (www.resgen.com)
 Seq primer: M13 Forward
 POLYA=Yes.

FEATURES

source

1. 364
 Location/Qualifiers
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-BS2-bdk-h-10-0-UI"
 /dev_stage="embryonic 13 dpc"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="UI-R-BS2"
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-BS2
 library is a subtracted library derived from 13 dpc whole
 embryo tissue. For a detailed description of the library
 from which this clone was derived, please visit our web
 site at ratest.eng.uiowa.edu. The subtraction has been
 previously described in (Bonaldo, Lennon and Soares,
 Genome Research 6:791-806, 1996)
 TAG_TISSUE=embryo at 13 dpc
 TAG_LIB=UI-R-BS2
 TAG_SEQ=AATCC"

ORIGIN

Query Match 72.7%; Score 16; DB 10; Length 364;
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;
 Mismatches 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CACTGGTCTTCTGTG 21

|||||
 Db 129 CACTGGTCTTCTGTG 114

RESULT 8

LOCUS

BF389025/c
 DEFINITION
 UI-R-Y0-mj-g-07-0-UI.s1 UI-R-Y0 Rattus norvegicus cDNA clone
 UI-R-Y0-mj-g-07-0-UI 3', mRNA sequence.

ACCESSION

BF389025

KEYWORDS

SOURCE

Rattus norvegicus

EST.

406 bp mRNA linear EST 11-FEB-1999

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 406)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 889548

COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soaresuiowa.edu

The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized Adult Eye library. cDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: clones will be available through Research Genetics

Seq primer: M13 Forward.

FEATURES

Location/Qualifiers
1..406
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clones="UI-R-Y0-mj-g-07-0-UI"
/dev_stages="adult"
/lab_host="DH10B (Life Technologies)"
/clone_libs="UI-R-Y0"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-Y0 library is a subtracted library derived from an individually-tagged normalized whole-eye (minus the lens) library. The driver for the subtraction consisted of a pool of all previous libraries (UI-R-A0, UI-R-A1, UI-R-E0, UI-R-E1, UI-R-C0, and UI-R-C1). The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-Y0) was constructed as follows: PCR amplified cDNA inserts from previous library clones from which 3' ESTs had been derived were used as a driver in a hybridization with the normalized whole-eye library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-Y0 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996)"

ORIGIN

Query Match 72.7%; Score 16; DB 9; Length 406;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CACTGGTCTCTTGTG 21
|||||

Db 129 CACTGGTCTCTTGTG 114

RESULT 9

BX307267 422 bp mRNA linear EST 19-DEC-2003

LOCUS BX307267

DEFINITION BX307267 AGENAE Rainbow trout multi-tissues subtracted library (tcay) Oncorhynchus mykiss cDNA clone tcay0017b.d.06 5prim, mRNA sequence.

ACCESSION BX307267

VERSION
KEYWORDS
SOURCE
ORGANISM

BX307267.1 GI:29587912

Oncorhynchus mykiss (rainbow trout)

Oncorhynchus mykiss

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Govoroun,M., Guiguen,Y. and Le Gac,F.
Construction and primary characterization of normalized cDNA libraries in rainbow trout, Oncorhynchus mykiss
Unpublished (2003)

INRA - SCRIBE
Campus de Beaulieu, RENNES cedex, 35042, France
Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
Email: Yann.Guiguen@beaulieu.rennes.inra.fr

Sequence cleaned of vector, adaptor and repetitions. Contact us at sigenasupport@jouy.inra.fr to obtain the chromatogram of this sequence.

Plate: 0017 row: d column: 6

FEATURES

Location/Qualifiers
1..422
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"

/clone="tcay0017b.d.06"
/tissue_type="adipose tissue, blood, brain, kidney, liver, muscle, ovary, pituitary, testis"
/dev_stage="from embryos to adults"
/lab_host="DH10B"
/clone_libs="AGENAE Rainbow trout multi-tissues subtracted library (tcay)"

/note="Vector: pT7T3D-pac; Rainbow trout multi-tissues - normalized + 1 subtraction (tcay); Clone distribution : AGENAE Resource centre. Francois PIUMI, Francois.piumi@jouy.inra.fr, INRA, CEA Radiobiologie et Etude du genome (IREG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex, FRANCE"

ORIGIN

Query Match 72.7%; Score 16; DB 13; Length 422;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CACTGGTCTCTTGTG 21
|||||

Db 223 CACTGGTCTCTTGTG 238

RESULT 10

LOCUS

BX307267 433 bp mRNA linear EST 27-MAR-2003

DEFINITION BX307267 Oncorhynchus mykiss cDNA, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BX307267.1 GI:29306607

Oncorhynchus mykiss (rainbow trout)

Oncorhynchus mykiss

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

GRASP Consortium, Davidson,W.S., Koop,B.F. and
http://web.uvic.ca/cbr/grasp.

A survey of Salmo salar transcripts from high complexity cDNA libraries
Unpublished (2002)

Contact: Koop BF

Centre for Biomedical Research
University of Victoria
PO Box 3020 STN CSC, Victoria BC, V8W 3N5, Canada
Tel: 250 472 4067
Fax: 250 472 4075
Email: bkoop@uvic.ca

Centre for Biomedical Research, University of Victoria cDNA
preparation and sequencing: Roberto Alberto, Marianne
Beetz-Sargent, Maura Busby, Peter Hunt, Linda McKinnel, BF Koop.
bioinformatics: Gordon D Brown.

FEATURES
source
1. .433
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/strain="Chilliwack River steelhead"
/db_xref="taxon:8022"
/clone_lib="Oncorhynchus mykiss Chilliwack River steelhead
whole"
/note="Vector: pBlueScriptIIISK+; Library Creator: Matthew
L Rise, BF Koop; Rainbow trout tissue contributors:
Robert Devlin (DFO, Vancouver, B.C.)"

ORIGIN
Query Match 72.7%; Score 16; DB 14; Length 433;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CACTGGCTCTCTGTG 21
|||||
Db 238 CACTGGCTCTCTGTG 223
|||||

RESULT 11
LOCUS CB495414
omykswel006021 Oncorhynchus mykiss Chilliwack River steelhead whole
Oncorhynchus mykiss cDNA, mRNA sequence.
CB495414.1 GI:29306640
EST.
Oncorhynchus mykiss (rainbow trout)

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 433)
http://web.uvic.ca/cbr/grasp.
A survey of Salmo salar transcripts from high complexity cDNA
libraries
Unpublished (2002)
Contact: Koop BF
Centre for Biomedical Research
University of Victoria
PO Box 3020 STN CSC, Victoria BC, V8W 3N5, Canada
Tel: 250 472 4067
Fax: 250 472 4075
Email: bkoop@uvic.ca
Centre for Biomedical Research, University of Victoria cDNA
preparation and sequencing: Roberto Alberto, Marianne
Beetz-Sargent, Maura Busby, Peter Hunt, Linda McKinnel, BF Koop.
bioinformatics: Gordon D Brown.

FEATURES
source
1. .433
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/strain="Chilliwack River steelhead"
/db_xref="taxon:8022"
/clone_lib="Oncorhynchus mykiss Chilliwack River steelhead
whole"
/note="Vector: pBlueScriptIIISK+; Library Creator: Matthew
L Rise, BF Koop; Rainbow trout tissue contributors:
Robert Devlin (DFO, Vancouver, B.C.)"

ORIGIN
Query Match 72.7%; Score 16; DB 14; Length 433;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CACTGGCTCTCTGTG 21
|||||
Db 238 CACTGGCTCTCTGTG 223
|||||

RESULT 11
LOCUS CB495414
omykswel006021 Oncorhynchus mykiss Chilliwack River steelhead whole
Oncorhynchus mykiss cDNA, mRNA sequence.
CB495414.1 GI:29306640
EST.
Oncorhynchus mykiss (rainbow trout)

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 433)
http://web.uvic.ca/cbr/grasp.
A survey of Salmo salar transcripts from high complexity cDNA
libraries
Unpublished (2002)
Contact: Koop BF
Centre for Biomedical Research
University of Victoria
PO Box 3020 STN CSC, Victoria BC, V8W 3N5, Canada
Tel: 250 472 4067
Fax: 250 472 4075
Email: bkoop@uvic.ca
Centre for Biomedical Research, University of Victoria cDNA
preparation and sequencing: Roberto Alberto, Marianne
Beetz-Sargent, Maura Busby, Peter Hunt, Linda McKinnel, BF Koop.
bioinformatics: Gordon D Brown.

FEATURES
source
1. .433
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/strain="Chilliwack River steelhead"
/db_xref="taxon:8022"
/clone_lib="Oncorhynchus mykiss Chilliwack River steelhead
whole"
/note="Vector: pBlueScriptIIISK+; Library Creator: Matthew
L Rise, BF Koop; Rainbow trout tissue contributors:
Robert Devlin (DFO, Vancouver, B.C.)"

ORIGIN
Query Match 72.7%; Score 16; DB 14; Length 433;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CACTGGCTCTCTGTG 21
|||||
Db 196 CACTGGCTCTCTGTG 211
|||||

RESULT 12
LOCUS CB495567
omykswel006066 Oncorhynchus mykiss Chilliwack River steelhead whole
Oncorhynchus mykiss cDNA, mRNA sequence.
CB495567
EST.
Oncorhynchus mykiss (rainbow trout)

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 433)
http://web.uvic.ca/cbr/grasp.
A survey of Salmo salar transcripts from high complexity cDNA
libraries
Unpublished (2002)
Contact: Koop BF
Centre for Biomedical Research
University of Victoria
PO Box 3020 STN CSC, Victoria BC, V8W 3N5, Canada
Tel: 250 472 4067
Fax: 250 472 4075
Email: bkoop@uvic.ca
Centre for Biomedical Research, University of Victoria cDNA
preparation and sequencing: Roberto Alberto, Marianne
Beetz-Sargent, Maura Busby, Peter Hunt, Linda McKinnel, BF Koop.
bioinformatics: Gordon D Brown.

FEATURES
source
1. .433
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/strain="Chilliwack River steelhead"
/db_xref="taxon:8022"
/clone_lib="Oncorhynchus mykiss Chilliwack River steelhead
whole"
/note="Vector: pBlueScriptIIISK+; Library Creator: Matthew
L Rise, BF Koop; Rainbow trout tissue contributors:
Robert Devlin (DFO, Vancouver, B.C.)"

ORIGIN
Query Match 72.7%; Score 16; DB 14; Length 433;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CACTGGCTCTCTGTG 21
|||||
Db 196 CACTGGCTCTCTGTG 211
|||||

RESULT 13
LOCUS BY505647/c
RIKEN full-length enriched, bone marrow macrophage Mus
musculus cDNA clone I830091A16 3', mRNA sequence.
BY505647
EST.
Mus musculus (house mouse)

ORGANISM
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 451)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaide, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojohori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Baralov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalia, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Karai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagaehima, T., Numata, K., Okido, T., Pavan, W.J., Perte, G., Pesole, G., Petkovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itch, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

22354683

12466851

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome.res@gsc.riken.go.jp

URL: <http://genome.gsc.riken.go.jp/>

Aizawa, K., Akimura, T., Arakawa, I., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission

Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by David A. Hume (Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane, Q 4072 Australia) whose assistance we gratefully acknowledge.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

Location/Qualifiers

source

1. .451

/organism="Mus musculus"

/mol_type="mRNA"

/strains="CS7BL/6J"

/db_xref="taxon:10090"

/clone="I830091A16"

/tissue_type="bone marrow"

/cell_type="macrophage"

/clone_lib="RIKEN full-length enriched, bone marrow macrophage"

ORIGIN

Query Match 72.7%; Score 16; DB 13; Length 451;

Best Local Similarity 100.0%; Pred. No. 6.8e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ACCACTGGCTCTCTTG 19

DB 351 ACCACTGGCTCTCTTG 336

RESULT 14

LOCUS BF388753 456 bp mRNA linear EST 27-NOV-2000

DEFINITION UI-R-BS2-bde-b-08-0-UI.s1 UI-R-BS2 Rattus norvegicus cDNA clone

ACCESSION BF388753

VERSION BF388753.1 GI:11373577

KEYWORDS EST.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

REFERENCE 1 (bases 1 to 456)

AUTHORS Ronaldo, M.F., Lennon, G. and Soares, M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene

JOURNAL discovery

MEDLINE 97044477

PUBMED 889548

COMMENT Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

The sequence contained an oligo-dT track that was present in the strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the normalized embryo at 13 dpc library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)

Seq primer: M13 Forward

POLYA=Yes.

Location/Qualifiers

1. .456

/organism="Rattus norvegicus"

/mol_type="mRNA"

/strains="Sprague-Dawley"

/db_xref="taxon:10116"

/clone="UI-R-BS2-bde-b-08-0-UI"

/dev_stage="embryonic 13 dpc"

/lab_host="DHI0B (Life Technologies)"

/clone_lib="UI-R-BS2"

/notes="Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-BS2 library is a subtracted library derived from 13 dpc whole embryo tissue. For a detailed description of the library from which this clone was derived, please visit our web

FEATURES

source

1. .456

/organism="Rattus norvegicus"

/mol_type="mRNA"

/strains="Sprague-Dawley"

/db_xref="taxon:10116"

/clone="UI-R-BS2-bde-b-08-0-UI"

/dev_stage="embryonic 13 dpc"

/lab_host="DHI0B (Life Technologies)"

/clone_lib="UI-R-BS2"

/notes="Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-BS2 library is a subtracted library derived from 13 dpc whole embryo tissue. For a detailed description of the library from which this clone was derived, please visit our web

site at ratseq.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
TAG_TISSUE=embryo at 13 dpc
TAG_LIB=UI-R-BS2
TAG_SEQ=AATCC"

ORIGIN

Query Match 72.7%; Score 16; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 CACTGGTCTTCTTG 21
|||||
DB 129 CACTGGTCTTCTTG 114

RESULT 15

BF402543/c 500 bp mRNA linear EST 28-NOV-2000
LOCUS
DEFINITION
UI-R-CA0-bhr-f-05-0-UI.s1 UI-R-CA0 Rattus norvegicus cDNA clone
UI-R-CA0-bhr-f-05-0-UI 3', mRNA sequence.

ACCESSION
BF402543
VERSION
BF402543.1 GI:11390518

KEYWORDS
EST.

SOURCE
Rattus norvegicus (Norway rat)

ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
1 (bases 1 to 500)

AUTHORS
Bonaldo, M.F., Lennon, G. and Soares, M.B.

TITLE
Normalization and subtraction: two approaches to facilitate gene

discovery

JOURNAL
Genome Res. 6 (9), 791-806 (1996)

MEDLINE
97044477

PUBMED
8889548

COMMENT
Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLVA=Yes.

FEATURES

Location/Qualifiers

1..500
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-CA0-bhr-f-05-0-UI"
/lab_host="DH10B (Life Technologies)"
/clone_lib="UI-R-CA0"
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; The UI-R-CA0 library is a subtracted library derived from the following tissues: thalamus, cerebellum, hypothalamus, medulla, pons, midbrain, cerebral cortex, corpus striatum, testis, and hippocampus. For a detailed description of the library from which this clone was derived, please visit our web site at ratseq.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
TAG_SEQ=None found"

ORIGIN

Query Match 72.7%; Score 16; DB 10; Length 500;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 CACTGGTCTTCTTG 21
|||||
DB 129 CACTGGTCTTCTTG 114

Search completed: August 2, 2004, 20:28:01

Job time : 912.207 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 18:10:40 ; Search time 22.1897 Seconds
(without alignments)
550.208 Million cell updates/sec

Title: US-10-068-067-18

Perfect score: 22

Sequence: 1 cttgtgcttaccgggcaagaa 22

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents, NA.*

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3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
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5: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	21	95.5	1193	4	US-08-720-565-3
2	14	63.6	1262	4	US-09-212-609B-29
3	14	63.6	1262	4	US-09-064-411A-31
4	14	63.6	1267	4	US-09-064-411A-22
5	14	63.6	1267	4	US-09-280-428A-9
6	14	63.6	1456	4	US-09-064-411A-23
7	14	63.6	1578	4	US-09-252-991A-5039
8	14	63.6	1581	4	US-09-252-991A-5177
9	13	59.1	24	3	US-08-943-731-498
10	13	59.1	511	3	US-08-943-731-441
11	13	59.1	905	4	US-09-221-017B-560
12	13	59.1	948	4	US-09-134-001C-949
13	13	59.1	987	4	US-09-543-681A-323
14	13	59.1	1197	4	US-09-489-039A-2370
15	13	59.1	3762	3	US-09-318-448-17
16	13	59.1	2183	3	US-08-943-731-3
17	13	59.1	3524	3	US-08-923-137-1
18	13	59.1	44848	4	US-09-435-739-42
19	13	59.1	72928	3	US-09-009-913-1
20	13	59.1	1830121	4	US-09-557-884-1
21	13	59.1	1830121	4	US-09-643-990A-1
22	12	54.5	99	3	US-08-995-156A-10
23	12	54.5	99	4	US-09-419-281-10
24	12	54.5	281	4	US-08-469-260A-18
25	12	54.5	281	4	US-08-469-260A-20
26	12	54.5	281	4	US-08-488-446-18
27	12	54.5	281	4	US-08-488-446-20

Sequence 18, Appl
Sequence 20, Appl
Sequence 114, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 3746, Ap
Sequence 409, App
Sequence 409, App
Sequence 409, App
Sequence 409, App
Sequence 409, App
Sequence 2525, Ap
Sequence 161, App
Sequence 161, App
Sequence 11017, A
Sequence 1044, Ap
Sequence 14394, A
Sequence 681, App

28 12 54.5 281 4 US-08-467-344A-18
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30 12 54.5 282 4 US-08-150-204B-114
31 12 54.5 285 3 US-08-995-156A-6
32 12 54.5 285 4 US-09-419-281-6
33 12 54.5 293 4 US-09-313-294A-3746
34 12 54.5 329 4 US-09-702-705-409
35 12 54.5 329 4 US-09-736-457-409
36 12 54.5 329 4 US-09-614-124B-409
37 12 54.5 329 4 US-09-671-325-409
38 12 54.5 329 4 US-09-589-184-409
39 12 54.5 351 4 US-09-252-991A-2525
40 12 54.5 396 4 US-09-640-173-161
41 12 54.5 396 4 US-09-713-550-161
42 12 54.5 403 4 US-09-621-976-11017
43 12 54.5 414 4 US-09-489-039A-1044
44 12 54.5 432 4 US-09-252-991A-14394
45 12 54.5 459 4 US-09-543-681A-681

ALIGNMENTS

RESULT 1
US-08-720-565-3
Sequence 3, Application US/08720565
Patent No. 6537764
GENERAL INFORMATION:
APPLICANT: Gerard, Craig J.
APPLICANT: Gerard, No. 6537764ma P.
APPLICANT: Mackay, Charles R.
APPLICANT: Ponath, Paul D.
APPLICANT: Post, Theodore W.
APPLICANT: Qin, Shixin
TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTOR GENE CCR3 AND
TITLE OF INVENTION: ANTAGONISTS THEREOF
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173

COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,565
FILING DATE: 30-SEP-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00608
FILING DATE: 19-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375,199
FILING DATE: 19-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS94-05A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1193 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna

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;
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; NAME/KEY: CDS
; LOCATION: 92..1156
US-08-720-565-3

Query Match          95.5%; Score 21; DB 4; Length 1193;
Best Local Similarity 100.0%; Pred. No. 0.00086;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 TTGTGCTTATCCGGGCAAGAA 22
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Db   1 TTGTGCTTATCCGGGCAAGAA 21

RESULT 2
US-09-212-609B-29/c
; Sequence 29, Application US/09212609B
; Patent No. 6323395
; GENERAL INFORMATION:
; APPLICANT: Rubin-Wilson, Beth C.
; APPLICANT: Young, Scott A.
; APPLICANT: Folkerts, Otto
; TITLE OF INVENTION: Nucleotide Sequences of Maize and Soybean
; TITLE OF INVENTION: Beta-Ketoacyl-Acyl Carrier Protein Synthase II and
; TITLE OF INVENTION: Their Use in the Regulation of Fatty Acid Content of
; TITLE OF INVENTION: Oil
; FILE REFERENCE: 50608
; CURRENT APPLICATION NUMBER: US/09/212,609B
; CURRENT FILING DATE: 1998-12-16
; PRIOR APPLICATION NUMBER: US 60/06874
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 1262
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:globulin
; OTHER INFORMATION: promoter
US-09-212-609B-29

Query Match          63.6%; Score 14; DB 4; Length 1262;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  4 GTGCTTATCCGGGC 17
    |||||
Db   1069 GTGCTTATCCGGGC 1056

RESULT 3
US-09-064-411A-31/c
; Sequence 31, Application US/09064411A
; Patent No. 6331664
; GENERAL INFORMATION:
; APPLICANT: Rubin-Wilson, Beth
; APPLICANT: Guo, Lining
; APPLICANT: Skokut, Tom
; APPLICANT: Young, Scott
; APPLICANT: Folkerts, Otto
; APPLICANT: Armstrong, Katherine
; APPLICANT: Cowen, Neil M.
; TITLE OF INVENTION: Nucleotide Sequences of Maize Oleoyl-ACP
; TITLE OF INVENTION: Thioesterase and Palmitoyl-ACP Thioesterase Genes and
; TITLE OF INVENTION: Their Use in the Regulation of Fatty Acid Content of Oil
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dow Agrosciences Patent Department
; STREET: 9330 Zionsville Road
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA

Query Match          63.6%; Score 14; DB 4; Length 1262;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  4 GTGCTTATCCGGGC 17
    |||||
Db   1069 GTGCTTATCCGGGC 1056

RESULT 4
US-09-064-411A-22/c
; Sequence 22, Application US/09064411A
; Patent No. 6331664
; GENERAL INFORMATION:
; APPLICANT: Rubin-Wilson, Beth
; APPLICANT: Guo, Lining
; APPLICANT: Skokut, Tom
; APPLICANT: Young, Scott
; APPLICANT: Folkerts, Otto
; APPLICANT: Armstrong, Katherine
; APPLICANT: Cowen, Neil M.
; TITLE OF INVENTION: Nucleotide Sequences of Maize Oleoyl-ACP
; TITLE OF INVENTION: Thioesterase and Palmitoyl-ACP Thioesterase Genes and
; TITLE OF INVENTION: Their Use in the Regulation of Fatty Acid Content of Oil
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dow Agrosciences Patent Department
; STREET: 9330 Zionsville Road
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA

Query Match          63.6%; Score 14; DB 4; Length 1262;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  4 GTGCTTATCCGGGC 17
    |||||
Db   1069 GTGCTTATCCGGGC 1056

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,411A
FILING DATE: 22-APR-1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Borucki, Andrea T.
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 50433
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-337-4846
TELEFAX: 317-337-4847
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 1262 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-064-411A-31
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;
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/064,411A
; FILING DATE: 22-APR-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/045,827
; FILING DATE: 05-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Borucki, Andrea T.
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 50433
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-337-4846
; TELEFAX: 317-337-4847
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1262 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-064-411A-31

Query Match          63.6%; Score 14; DB 4; Length 1262;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  4 GTGCTTATCCGGGC 17
    |||||
Db   1069 GTGCTTATCCGGGC 1056

RESULT 4
US-09-064-411A-22/c
; Sequence 22, Application US/09064411A
; Patent No. 6331664
; GENERAL INFORMATION:
; APPLICANT: Rubin-Wilson, Beth
; APPLICANT: Guo, Lining
; APPLICANT: Skokut, Tom
; APPLICANT: Young, Scott
; APPLICANT: Folkerts, Otto
; APPLICANT: Armstrong, Katherine
; APPLICANT: Cowen, Neil M.
; TITLE OF INVENTION: Nucleotide Sequences of Maize Oleoyl-ACP
; TITLE OF INVENTION: Thioesterase and Palmitoyl-ACP Thioesterase Genes and
; TITLE OF INVENTION: Their Use in the Regulation of Fatty Acid Content of Oil
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dow Agrosciences Patent Department
; STREET: 9330 Zionsville Road
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/064,411A
; FILING DATE: 22-APR-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Borucki, Andrea T.
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 50433
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-337-4846
; TELEFAX: 317-337-4847
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1262 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-064-411A-31
```


ATTORNEY/AGENT INFORMATION:
NAME: Borucki, Andrea T.
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 50433
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-337-4846
TELEFAX: 317-337-4847
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 1267 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-064-411A-22

Query Match 63.6%; Score 14; DB 4; Length 1267;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTGCTTATCCGGC 17
Db 1074 GTGCTTATCCGGC 1061

RESULT 5
US-09-280-428A-9/c
Sequence 9, Application US/09280428A
Patent No. 6495738
GENERAL INFORMATION:
APPLICANT: Folkerts, Otto
APPLICANT: Merlo, Donald J
TITLE OF INVENTION: Modification of Fatty Acid Composition in Plants by
TITLE OF INVENTION: Expression of A Fungal Acyl-CoA Desaturase
FILE REFERENCE: 50612
CURRENT APPLICATION NUMBER: US/09/280,428A
CURRENT FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: 60/079840
PRIOR FILING DATE: 1998-03-30
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 9
LENGTH: 1267
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: portion of
OTHER INFORMATION: pGKN62-2
US-09-280-428A-9

Query Match 63.6%; Score 14; DB 4; Length 1267;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTGCTTATCCGGC 17
Db 1074 GTGCTTATCCGGC 1061

RESULT 6
US-09-064-411A-23/c
Sequence 23, Application US/09064411A
Patent No. 6331664
GENERAL INFORMATION:
APPLICANT: Rubin-Wilson, Beth
APPLICANT: Guo, Lining
APPLICANT: Skokut, Tom
APPLICANT: Young, Scott
APPLICANT: Folkerts, Otto
APPLICANT: Armstrong, Katherine
APPLICANT: Cowen, Neil M.
TITLE OF INVENTION: Nucleotide Sequences of Maize Oleoyl-ACP
TITLE OF INVENTION: Thioesterase and Palmitoyl-ACP Thioesterase Genes and

TITLE OF INVENTION: Their Use In The Regulation of Fatty Acid Content of Oil
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSER: Dow AgroSciences Patent Department
STREET: 9330 Zionsville Road
CITY: Indianapolis
STATE: Indiana
COUNTRY: USA
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,411A
FILING DATE: 22-APR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/045,827
FILING DATE: 05-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Borucki, Andrea T.
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 50433
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-337-4846
TELEFAX: 317-337-4847
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 1456 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-064-411A-23

Query Match 63.6%; Score 14; DB 4; Length 1456;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTGCTTATCCGGC 17
Db 1265 GTGCTTATCCGGC 1252

RESULT 7
US-09-252-991A-5039/c
Sequence 5039, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 5039
LENGTH: 1578
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5039

Query Match 63.6%; Score 14; DB 4; Length 1578;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CTTATCCGGCAAG 20

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Db 425 CTTATCGGCGCAG 412
|||||
RESULT 8
US-09-252-991A-5177
; Sequence 5177, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5177
; LENGTH: 1581
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5177

Query Match 63.6%; Score 14; DB 4; Length 1581;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CTTATCGGCGCAG 20
|||||
Db 1247 CTTATCGGCGCAG 1260
|||||

RESULT 9
US-08-943-731-498
; Sequence 498, Application US/08943731
; Patent No. 6265157
; GENERAL INFORMATION:
; APPLICANT: PROCKOP, DARWIN J.
; APPLICANT: SPOTILA, LORETTA D.
; APPLICANT: DELTAS, CONSTANTINOS D.
; APPLICANT: SEREDA, LARISA
; APPLICANT: LARSON, ANDREA W.
; APPLICANT: PACK, MICHAEL
; APPLICANT: COLIGE, ALAIN
; APPLICANT: EARLY, JAMES
; APPLICANT: KORKKO, JARMO
; APPLICANT: ALA-KOKKO, LEENA, et al.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
; TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
; NUMBER OF SEQUENCES: 666
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
; STREET: FLR.
; CITY: PHILADELPHIA
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-7086
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,731
; FILING DATE: 03-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,322
; FILING DATE: 14-MAR-1994

Db 1247 CTTATCGGCGCAG 1260
|||||

Query Match 63.6%; Score 14; DB 4; Length 1581;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CTTATCGGCGCAG 20
|||||
Db 1247 CTTATCGGCGCAG 1260
|||||

RESULT 9
US-08-943-731-498
; Sequence 498, Application US/08943731
; Patent No. 6265157
; GENERAL INFORMATION:
; APPLICANT: PROCKOP, DARWIN J.
; APPLICANT: SPOTILA, LORETTA D.
; APPLICANT: DELTAS, CONSTANTINOS D.
; APPLICANT: SEREDA, LARISA
; APPLICANT: LARSON, ANDREA W.
; APPLICANT: PACK, MICHAEL
; APPLICANT: COLIGE, ALAIN
; APPLICANT: EARLY, JAMES
; APPLICANT: KORKKO, JARMO
; APPLICANT: ALA-KOKKO, LEENA, et al.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
; TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
; NUMBER OF SEQUENCES: 666
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
; STREET: FLR.
; CITY: PHILADELPHIA
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-7086
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,731
; FILING DATE: 03-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,322
; FILING DATE: 14-MAR-1994
```

```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/803,628
; FILING DATE: 03-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: DOYLE LEARY PH.D., KATHRYN
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: 9598-27
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-565-1284
; TELEFAX: 215-567-2991
; TELEX: 831-494
; INFORMATION FOR SEQ ID NO: 498:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-943-731-498

Query Match 59.1%; Score 13; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGTGCTTATCC 13
|||||
Db 12 CTTGTGCTTATCC 24
|||||

RESULT 10
US-08-943-731-141
; Sequence 141, Application US/08943731
; Patent No. 6265157
; GENERAL INFORMATION:
; APPLICANT: PROCKOP, DARWIN J.
; APPLICANT: SPOTILA, LORETTA D.
; APPLICANT: DELTAS, CONSTANTINOS D.
; APPLICANT: SEREDA, LARISA
; APPLICANT: LARSON, ANDREA W.
; APPLICANT: PACK, MICHAEL
; APPLICANT: COLIGE, ALAIN
; APPLICANT: EARLY, JAMES
; APPLICANT: KORKKO, JARMO
; APPLICANT: ALA-KOKKO, LEENA, et al.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
; TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
; NUMBER OF SEQUENCES: 666
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
; STREET: FLR.
; CITY: PHILADELPHIA
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-7086
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,731
; FILING DATE: 03-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,322
; FILING DATE: 14-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/803,628
; FILING DATE: 03-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: DOYLE LEARY PH.D., KATHRYN
; REGISTRATION NUMBER: 36,317
```

; REFERENCE/DOCKET NUMBER: 9598-27
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-965-1284
; TELEFAX: 215-567-2991
; TELEX: 831-494
; INFORMATION FOR SEQ ID NO: 141:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 511 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-943-731-141

Query Match 59.1%; Score 13; DB 3; Length 511;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTGTGCTTATCC 13
Db 421 CTTGTGCTTATCC 433

RESULT 11

US-09-221-017B-560/c
; Sequence 560, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:

; APPLICANT: Ross, Bruce C.
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF

; NUMBER OF SEQUENCES: 1120

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORRISON & FOERSTER

; STREET: 755 PAGE MILL ROAD

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304-1018

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows

; SOFTWARE: FASTSEQ for Windows Version 2.0b

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/221,017B

; FILING DATE: 23-DEC-1998

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PP1182

; FILING DATE: 31-DEC-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PP1546

; FILING DATE: 30-JAN-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PP2911

; FILING DATE: 09-APR-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/AU98/01023

; FILING DATE: 10-DEC-1998

; ATTORNEY/AGENT INFORMATION:

; NAME: Monroy, Gladys H

; REGISTRATION NUMBER: 32,430

; REFERENCE/DOCKET NUMBER: 27340-20021.00

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-813-5600

; TELEFAX: 650-494-0792

; TELEX: 706141

; INFORMATION FOR SEQ ID NO: 560:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 905 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: circular

; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: UNKNOWN
; ORIGINAL SOURCE:
; ORGANISM: PORPHYROMONAS GINGIVALIS
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1...905
US-09-221-017B-560

Query Match 59.1%; Score 13; DB 4; Length 905;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TATCCGGGCAAGA 21
Db 547 TATCCGGGCAAGA 535

RESULT 12

US-09-134-001C-949
; Sequence 949, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC-007

; CURRENT APPLICATION NUMBER: US/09/134,001C

; CURRENT FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/064,964

; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: US 60/055,779

; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 5674

; SEQ ID NO 949

; LENGTH: 948

; TYPE: DNA

; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-949

Query Match 59.1%; Score 13; DB 4; Length 948;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GTGCTTATCCGGG 16
Db 476 GTGCTTATCCGGG 488

RESULT 13

US-09-543-681A-323
; Sequence 323, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:

; APPLICANT: GARY BRETON

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS

; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 2709.1002-001

; CURRENT APPLICATION NUMBER: US/09/543,681A

; CURRENT FILING DATE: 2000-04-05

; PRIOR APPLICATION NUMBER: US 60/128,706

; PRIOR FILING DATE: 1999-04-09

; NUMBER OF SEQ ID NOS: 8344

; SEQ ID NO 323

; LENGTH: 987

; TYPE: DNA

; ORGANISM: Proteus mirabilis

US-09-543-681A-323

Query Match 59.1%; Score 13; DB 4; Length 987;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTGCTTATCCGGG 16
| | | | | | | | | |
Db 521 GTGCTTATCCGGG 533

RESULT 14

US-09-489-039A-2370
; Sequence 2370, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 2370
; LENGTH: 1197
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-2370

Query Match 59.1%; Score 13; DB 4; Length 1197;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GCTTATCCGGGCA 18
| | | | | | | | | |
Db 321 GCTTATCCGGGCA 333

RESULT 15

US-09-318-448-17/c
; Sequence 17, Application US/09318448
; Patent No. 6210950
; GENERAL INFORMATION:
; APPLICANT: Johnson, William G.
; APPLICANT: Stenroos, Edward S.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
; FILE REFERENCE: 601-1-057
; CURRENT APPLICATION NUMBER: US/09/318,448
; CURRENT FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 3762
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-318-448-17

Query Match 59.1%; Score 13; DB 3; Length 3762;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGTGCTTATCC 13
| | | | | | | | | |
Db 2217 CTTGTGCTTATCC 2205

Search completed: August 2, 2004, 20:30:05
Job time : 24.1897 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 16:56:38 ; Search time 106.207 Seconds

(without alignments)
879.984 Million cell updates/sec

Title: US-10-068-067-18

Perfect score: 22

Sequence: 1 cttgtccttaccgggcaagaa 22

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 337863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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5: geneseqn2001bs.*

6: geneseqn2002s.*

7: geneseqn2003as.*

8: geneseqn2003bs.*

9: geneseqn2003cs.*

10: geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	22	ABQ78516	ABQ78516 Nucleotid
2	22	100.0	22	ABQ78521	ABQ78521 Nucleotid
3	22	100.0	51	ABQ78514	ABQ78514 Nucleotid
4	22	100.0	51	ABQ78519	ABQ78519 Nucleotid
5	22	100.0	2895	ABQ78513	ABQ78513 Nucleotid
6	21	95.5	1193	AAT31335	AAT31335 CC-Chemok
7	21	95.5	1193	AAV07403	AAV07403 Human C-C
8	16	72.7	265	ABX50975	ABX50975 Bovine ES
9	15	68.2	23654	AB117664	AB117664 Drosophila
10	14	63.6	438	AB12176	AB12176 Alloioococ
11	14	63.6	717	ABK75795	ABK75795 Bacillus
12	14	63.6	945	AAK91767	AAK91767 Porphyrom
13	14	63.6	987	AAK91633	AAK91633 Porphyrom
14	14	63.6	1262	AAV80227	AAV80227 Maize glo
15	14	63.6	1262	ABA94959	ABA94959 Globulin
16	14	63.6	1267	AAV80218	AAV80218 Maize glo
17	14	63.6	1267	AAK90960	AAK90960 Nucleotid
18	14	63.6	1432	AAK57151	AAK57151 Maize glo
19	14	63.6	1456	AAV80219	AAV80219 Maize glo
20	14	63.6	2235	ADP48617	ADP48617 Rat gene
21	14	63.6	2331	AD312180	AD312180 Alloioococ
22	14	63.6	2331	AD312178	AD312178 Alloioococ
23	14	63.6	3017	AAK86511	AAK86511 DNA const

24	14	63.6	3408	7	ABT17984	Abt17984 Aspergill
25	14	63.6	3409	7	ABT19798	Abt19798 Aspergill
26	14	63.6	5511	2	AZ08718	Az08718 Chimeric
27	14	63.6	54382	8	AD312064_17	Continuation (18 o
28	13	59.1	24	5	AA522266	AA522266 Human COL
29	13	59.1	193	6	ABN73948	ABN73948 Bovine em
30	13	59.1	215	4	AAK79563	AAK79563 Human imm
31	13	59.1	228	5	AA569713	AA569713 DNA encod
32	13	59.1	260	6	AB179816	Ab179816 Human ova
33	13	59.1	375	7	ACA43197	ACA43197 Prokaryot
34	13	59.1	411	6	ABN70758	ABN70758 Streptoco
35	13	59.1	420	6	ABK78358	ABK78358 Bacillus
36	13	59.1	425	8	ACH40149	ACH40149 Human foe
37	13	59.1	492	6	ABN26019	ABN26019 Human ORF
38	13	59.1	493	9	ADE81829	ADE81829 Arabidops
39	13	59.1	511	5	AA521909	AA521909 Human COL
40	13	59.1	537	3	AA536765	AA536765 Arabidops
41	13	59.1	539	4	AA558713	AA558713 cDNA #138
42	13	59.1	566	8	ACH39350	ACH39350 Human foe
43	13	59.1	671	6	ABK29826	ABK29826 Colon ade
44	13	59.1	690	6	AA148404	AA148404 Human ser
45	13	59.1	690	6	AA344463	AA344463 Human ser

ALIGNMENTS

RESULT 1

ABQ78516

ID ABQ78516 standard; DNA; 22 BP.

XX AC ABQ78516;

XX AC

DT 25-NOV-2002 (first entry)

XX DE Nucleotide sequence of a regulatory sequence for human CCR3.

XX DE Human, CC chemokine receptor 3; CCR3; allergic disorder; probe;

KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;

KW infectious disorder; HIV; respiratory syncytial virus infection; ss.

XX OS Homo sapiens.

XX PN WC200262848-A2.

XX PD 15-AUG-2002.

XX PF 06-FEB-2002; 2002WO-US003442.

XX PR 07-FEB-2001; 2001US-0267073P.

XX PR 05-FEB-2002; 2002US-00068067.

(CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

Rothenberg ME, Zimmerman N;

WPI; 2002-657524/70.

New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated

exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable

of binding to regulatory elements, useful for preventing e.g. allergic

inflammatory reactions.

Claim 6; Page 54; 56pp; English.

The present sequence represents a probe for the human CC chemokine

receptor 3 (CCR3) gene. The probe is a regulatory sequence for CCR3. CCR3

is expressed on cells involved in allergic and/or inflammatory disorders.

The gene comprises 4 exons, with the coding region present on exon 4. The

specification describes methods of regulating the expression of CCR3. The

regulatory site is derived from an untranslated exon 1, exon 2, exon 3 or

promoter of a human CCR3 gene. Regulating the expression of the chemokine

receptor CCR3 is useful for preventing or treating disorders involving

CC eosinophils, such as allergic inflammatory and hypersensitivity
 CC reactions, certain types of leukemia, and certain infectious disorders
 CC involving CCR3, e.g. HIV or respiratory syncytial virus infection.
 CC Expression and modulation of CCR3 is a useful tool in assessing
 CC eosinophil targeting and in regulating eosinophil-mediated reactions and
 CC diseases
 XX
 SQ Sequence 22 BP; 5 A; 5 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 6; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.0016;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGTGCTTATCCGGGCAAGAA 22
 |||||
 Db 1 CTTGTGCTTATCCGGGCAAGAA 22

RESULT 2
 ABQ78521
 ID ABQ78521 standard; RNA; 22 BP.
 XX
 AC ABQ78521;

DT 25-NOV-2002 (first entry)

DE Nucleotide sequence of a regulatory sequence for human CCR3.

KW Human; CC chemokine receptor 3; CCR3; allergic disorder; probe;
 KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;
 KW infectious disorder; HIV; respiratory syncytial virus infection; ss.

XX Homo sapiens.
 XX WO200262848-A2.
 XX
 XX 15-AUG-2002.

PF 06-FEB-2002; 2002WO-US003442.

PR 07-FEB-2001; 2001US-0267073P.

PR 05-FEB-2002; 2002US-00068067.

XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

PA Rothenberg ME, Zimmermann N;

PI WPI; 2002-657524/70.

DR New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated
 XX exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable
 XX of binding to regulatory elements, useful for preventing e.g. allergic
 XX inflammatory reactions.

PS Claim 8; Page 56; 56pp; English.

XX The present sequence represents a probe for the human CC chemokine
 XX receptor 3 (CCR3) gene. The probe is a regulatory sequence for CCR3. CCR3
 CC is expressed on cells involved in allergic and/or inflammatory disorders.
 CC The gene comprises 4 exons, with the coding region present on exon 4. The
 CC specification describes methods of regulating the expression of CCR3. The
 CC regulatory site is derived from an untranslated exon 1, exon 2, exon 3 or
 CC promoter of a human CCR3 gene. Regulating the expression of the chemokine
 CC receptor CCR3 is useful for preventing or treating disorders involving
 CC eosinophils, such as allergic inflammatory and hypersensitivity
 CC reactions, certain types of leukemia, and certain infectious disorders
 CC involving CCR3, e.g. HIV or respiratory syncytial virus infection.
 CC Expression and modulation of CCR3 is a useful tool in assessing
 CC eosinophil targeting and in regulating eosinophil-mediated reactions and
 CC diseases

XX Sequence 22 BP; 5 A; 5 C; 6 G; 0 T; 6 U; 0 Other;

Query Match 100.0%; Score 22; DB 6; Length 22;
 Best Local Similarity 72.7%; Pred. No. 0.0016;
 Matches 16; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGTGCTTATCCGGGCAAGAA 22
 |||||
 Db 1 CUUGUGCUUATCCGGGCAAGAA 22

RESULT 3
 ABQ78514
 ID ABQ78514 standard; DNA; 51 BP.
 XX
 AC ABQ78514;

DT 25-NOV-2002 (first entry)

DE Nucleotide sequence of a regulatory sequence for human CCR3.

KW Human; CC chemokine receptor 3; CCR3; allergic disorder; probe;
 KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;
 KW infectious disorder; HIV; respiratory syncytial virus infection; ss.

XX Homo sapiens.

XX
 XX Key Location/Qualifiers
 FT misc_binding 24..27
 FT /*tag= a

FT /note= "transcription factor binding site for GATA"

FT misc_binding 40..43

FT /*tag= b

FT /note= "transcription factor binding site for GATA"

XX WO200262848-A2.

XX 15-AUG-2002.

XX 06-FEB-2002; 2002WO-US003442.

XX 07-FEB-2001; 2001US-0267073P.

XX 05-FEB-2002; 2002US-00068067.

XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

XX Rothenberg ME, Zimmermann N;

XX WPI; 2002-657524/70.

XX New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated
 XX exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable
 XX of binding to regulatory elements, useful for preventing e.g. allergic
 XX inflammatory reactions.

PS Claim 2; Page 25; 56pp; English.

XX The present sequence represents a probe for the human CC chemokine
 XX receptor 3 (CCR3) gene. The probe comprises +10 to +60 of exon 1 of CCR3,
 CC and is a regulatory sequence for CCR3. CCR3 is expressed on cells
 CC involved in allergic and/or inflammatory disorders. The gene comprises 4
 CC exons, with the coding region present on exon 4. The specification
 CC describes methods of regulating the expression of CCR3. The regulatory
 CC site is derived from an untranslated exon 1, exon 2, exon 3 or promoter
 CC of a human CCR3 gene. Regulating the expression of the chemokine receptor
 CC CCR3 is useful for preventing or treating disorders involving
 CC eosinophils, such as allergic inflammatory and hypersensitivity
 CC reactions, certain types of leukemia, and certain infectious disorders
 CC involving CCR3, e.g. HIV or respiratory syncytial virus infection.
 CC Expression and modulation of CCR3 is a useful tool in assessing
 CC eosinophil targeting and in regulating eosinophil-mediated reactions and
 CC diseases

XX Sequence 51 BP; 13 A; 12 C; 11 G; 15 T; 0 U; 0 Other;

```

Query Match      100.0%; Score 22; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGTGCTTATCCGGCAAGAA 22
DB 16 CTTGTGCTTATCCGGCAAGAA 37

RESULT 4
ABQ78519
ID ABQ78519 standard; RNA; 51 BP.
XX
AC ABQ78519;
XX
DT 25-NOV-2002 (first entry)
XX
DE Nucleotide sequence of a regulatory sequence for human CCR3.
XX
KW Human; CC chemokine receptor 3; CCR3; allergic disorder; probe;
KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;
KW infectious disorder; HIV; respiratory syncytial virus infection; ss.
XX
OS Homo sapiens.
XX
FN WO200262848-A2.
XX
PD 15-AUG-2002.
XX
PF 06-FEB-2002; 2002WO-US003442.
XX
PR 07-FEB-2001; 2001US-0267073P.
XX
PR 05-FEB-2002; 2002US-00068067.
XX
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
XX
PI Rothenberg ME, Zimmerman N;
XX
DR WPI; 2002-657524/70.
XX
PT New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated
PT exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable
PT of binding to regulatory elements, useful for preventing e.g. allergic
PT inflammatory reactions.
XX
PS Claim 7; Page 56; 56pp; English.
XX
CC The present sequence represents a probe for the human CC chemokine
CC receptor 3 (CCR3) gene. The probe is a regulatory sequence for CCR3. CCR3
CC is expressed on cells involved in allergic and/or inflammatory disorders.
CC The gene comprises 4 exons, with the coding region present on exon 4. The
CC specification describes methods of regulating the expression of CCR3. The
CC regulatory site is derived from an untranslated exon 1, exon 2, exon 3 or
CC promoter of a human CCR3 gene. Regulating the expression of the chemokine
CC receptor CCR3 is useful for preventing or treating disorders involving
CC eosinophils, such as allergic inflammatory and hypersensitivity
CC reactions, certain types of leukemia, and certain infectious disorders
CC involving CCR3, e.g. HIV or respiratory syncytial virus infection.
CC Expression and modulation of CCR3 is a useful tool in assessing
CC eosinophil targeting and in regulating eosinophil-mediated reactions and
CC diseases
XX
SQ Sequence 51 BP; 13 A; 12 C; 11 G; 0 T; 15 U; 0 Other;

Query Match      100.0%; Score 22; DB 6; Length 51;
Best Local Similarity 72.7%; Pred. No. 0.0016;
Matches 16; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGTGCTTATCCGGCAAGAA 22
DB 16 CUUGGCUUACCGGCAAGAA 37

```

```

RESULT 5
ABQ78513
ID ABQ78513 standard; DNA; 2895 BP.
XX
AC ABQ78513;
XX
DT 25-NOV-2002 (first entry)
XX
DE Nucleotide sequence of the human CCR3 gene promoter.
XX
KW Human; CC chemokine receptor 3; CCR3; allergic disorder;
KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;
KW infectious disorder; HIV; respiratory syncytial virus infection;
KW promoter; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT misc_signal 1640..1645
FT /*tag= a
FT /*note= "splice donor consensus site"
XX
PN WO200262848-A2.
XX
XX 15-AUG-2002.
XX
XX 06-FEB-2002; 2002WO-US003442.
XX
XX 07-FEB-2001; 2001US-0267073P.
XX
XX 05-FEB-2002; 2002US-00068067.
XX
XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
XX
XX Rothenberg ME, Zimmerman N;
XX
XX WPI; 2002-657524/70.
XX
XX New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated
XX exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable
XX of binding to regulatory elements, useful for preventing e.g. allergic
XX inflammatory reactions.
XX
XX Disclosure; Fig 4; 56pp; English.
XX
CC The present sequence represents the promoter of the human CC chemokine
CC receptor 3 (CCR3) gene. CCR3 is expressed on cells involved in allergic
CC and/or inflammatory disorders. The gene comprises 4 exons, with the
CC coding region present on exon 4. The specification describes methods of
CC regulating the expression of CCR3. The regulatory site is derived from an
CC untranslated exon 1, exon 2, exon 3 or promoter of a human CCR3 gene.
CC Regulating the expression of the chemokine receptor CCR3 is useful for
CC preventing or treating disorders involving eosinophils, such as allergic
CC inflammatory and hypersensitivity reactions, certain types of leukemia,
CC and certain infectious disorders involving CCR3, e.g. HIV or respiratory
CC syncytial virus infection. Expression and modulation of CCR3 is a useful
CC tool in assessing eosinophil targeting and in regulating eosinophil-
CC mediated reactions and diseases
XX
SQ Sequence 2895 BP; 829 A; 590 C; 556 G; 920 T; 0 U; 0 Other;

Query Match      100.0%; Score 22; DB 6; Length 2895;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGTGCTTATCCGGCAAGAA 22
DB 1576 CTTGTGCTTATCCGGCAAGAA 1597

RESULT 6
AAT31335
ID AAT31335 standard; cDNA; 1193 BP.
XX

```

AC AAT31335;
 XX
 DT 15-NOV-1996 (first entry)
 XX
 DE CC-chemokine receptor 3 cDNA clone.
 XX
 KW CC-chemokine receptor 3; CKP-3; Eos-L2; inhibitor; antisense;
 KW antiinflammatory; eosinophil; ss.
 XX
 CS Homo sapiens.
 XX
 XX
 FH Key Location/Qualifiers
 FT CDS 92..1159
 FT /*tag= a
 FT variation 918..919
 FT /*tag= b
 FT /note= "CKR-3 cDNA clone has GC at positions 918-919,
 FT coding for serine (AGC) at position 276; a genomic clone
 FT has GC at these positions, coding for threonine (AGC)"
 XX
 XX WO9622371-A2.
 XX
 XX 25-JUL-1996.
 XX
 XX 19-JAN-1996; 96WO-US000608.
 XX
 XX 19-JAN-1995; 95US-00375199.
 XX
 XX (LEUK-) LEUKOSITE INC.
 XX (BGHM) BRIGHAM & WOMENS HOSPITAL.
 XX (CHIL-) CHILDRENS MEDICAL CENT.
 XX
 XX Gerard CU, Gerard NP, Mackay CR, Ponath PD, Post TW, Qin S;
 XX
 XX WPI: 1996-354528/35.
 XX P-PSDB; AAW03377.
 XX
 XX Mammalian chemokine receptor-3 and related nucleic acids - useful to
 XX identify receptor inhibitors to treat inflammatory disease, e.g.
 XX autoimmune disorders, certain cancers, etc.
 XX
 XX Claim 1; Page 111-113; 153pp; English.
 XX
 XX A genomic DNA clone (AAT31335) codes for a novel receptor (AAW03377),
 XX designated Eos L2 or C-C chemokine receptor 3 (CKR-3), involved in
 XX leukocyte migration associated with inflammation. It was isolated from a
 XX human library constructed from eosinophils obtd. from a patient with
 XX hyper-eosinophilic syndrome using a probe (p4 cDNA) encoding the MIP-
 XX 1alpha/RANTES receptor. A CKR-3 genomic clone (AAT31334) was also
 XX isolated, and a consensus sequence is given in AAT31336. The cDNA and
 XX genomic clones can be used for the prodn. of recombinant CKR-3 in host
 XX cells, or to design antisense sequences useful for treating inflammatory
 XX disease
 XX
 XX Sequence 1193 BP; 274 A; 310 C; 275 G; 334 T; 0 U; 0 Other;
 XX
 XX Query Match 95.5%; Score 21; DB 2; Length 1193;
 XX Best Local Similarity 100.0%; Fred. NO. 0.006;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 2 TTGTGCTTATCCGGCAAGAA 22
 XX |||||
 XX Db 1 TTGTGCTTATCCGGCAAGAA 21
 XX
 XX RESULT 7
 XX AAW07403
 XX ID AAW07403 standard; cDNA; 1193 BP.
 XX
 XX AC AAW07403;
 XX
 XX 28-SEP-1998 (first entry)
 XX
 XX

DE Human C-C chemokine receptor 3 cDNA.
 XX
 XX C-C chemokine receptor 3; CKR-3; CCR3; Eos L2; human;
 KW G protein-coupled receptor; leukocyte; antibody; antagonist;
 DE inflammation; allergy; asthma; graft rejection; infection;
 KW autoimmune disease; drug screening; therapy; ds.
 XX
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH CDS 92..1159
 FT /*tag= a
 XX
 XX WO9814480-A1.
 XX
 XX 09-APR-1998.
 XX
 XX 24-SEP-1997; 97WO-US017103.
 XX
 XX 30-SEP-1996; 96US-00720565.
 XX
 XX (LEUK-) LEUKOSITE INC.
 XX
 XX Mackay CR, Ponath PD;
 XX
 XX WPI: 1998-286418/25.
 XX P-PSDB; AAW51745.
 XX
 XX Antibodies to chemokine receptor-3 protein - useful for diagnosis and
 XX treatment of inflammatory conditions, e.g. allergy, asthma, autoimmune
 XX disease, graft rejection or cancer.
 XX
 XX Example 8; Page 134-136; 185pp; English.
 XX
 XX This cDNA codes for novel human C-C chemokine receptor 3 (see AAW51745);
 XX also designated CKR-3, CCR3 or Eos L2, that binds and mediates chemotaxis
 XX in response to chemokines such as eotaxin, RANTES and MCP-3. The cDNA was
 XX isolated from a human eosinophil cDNA library constructed from
 XX eosinophils obtained from a patient with hyper-eosinophilic syndrome, and
 XX using CKR-1 cDNA as probe. A genomic DNA sequence (see AAW07402) is also
 XX provided as well as a consensus sequence (see AAW07404) for CKR-3. The
 XX invention relates to isolated and/or recombinant nucleic acids encoding
 XX CKR-3, isolated or recombinant CKR-3 polypeptides, recombinant nucleic
 XX acid constructs, host cells useful for production of recombinant CKR-3
 XX proteins, to antibodies reactive with the receptors, and to methods of
 XX using these products to identify ligands, antagonists and agonists of
 XX receptor function. Inhibitors of CKR-3 can be used to treat: inflammatory
 XX or allergic diseases and conditions, including respiratory allergic
 XX diseases such as asthma, allergic rhinitis, hypersensitivity lung
 XX disease, hypersensitivity pneumonitis, eosinophilic pneumonia (e.g.
 XX Loeffler's syndrome, chronic eosinophilic pneumonia, interstitial lung
 XX disease (ILD) e.g. idiopathic pulmonary fibrosis or ILD associated with
 XX rheumatoid arthritis, systemic lupus erythematosus, ankylosing
 XX spondylitis, systemic sclerosis, Sjogren's syndrome, polymyositis or
 XX dermatomyositis), systemic anaphylaxis or hypersensitivity responses,
 XX drug allergy, insect sting allergy, inflammatory bowel disease, such as
 XX Crohn's disease and ulcerative colitis, spondyloarthritis, scleroderma,
 XX psoriasis, inflammatory dermatosis such as dermatitis, eczema, atopic
 XX dermatitis, allergic contact dermatitis, urticaria, vasculitis (e.g.
 XX necrotizing, cutaneous and hypersensitivity vasculitis); eosinophilic
 XX myositis and eosinophilic fasciitis; autoimmune diseases such as
 XX rheumatoid arthritis, psoriatic arthritis, multiple sclerosis, systemic
 XX lupus erythematosus, myasthenia gravis, juvenile onset diabetes, graft
 XX glomerulonephritis, autoimmune thyroiditis and Behcet's disease; graft
 XX rejection, including allograft rejection or graft-versus-host disease;
 XX cancers with leukocyte infiltration of the skin or organs; and also
 XX reperfusion injury, atherosclerosis, certain haematologic malignancies,
 XX septic shock and endotoxin shock. Promoters of CKR-3 function can be used
 XX for treating: immunosuppression e.g. in AIDS patients or individuals
 XX undergoing radiation therapy, chemotherapy, therapy for autoimmune
 XX disease or other drug therapy, and immunosuppression due congenital
 XX deficiency in receptor function or other causes; and infectious diseases
 XX such as parasitic diseases, including helminth infections, such as

CC nematodes (round worms). The agents can also be used for detection and
CC diagnosis
XX
SQ Sequence 1193 BP; 274 A; 310 C; 275 G; 334 T; 0 U; 0 Other;
Query Match 95.5%; Score 21; DB 2; Length 1193;
Best Local Similarity 100.0%; Pred. No. 0.006;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TTGTGCTTATCGGGCAAGAA 22
DB 1 TTGTGCTTATCGGGCAAGAA 21
RESULT 8
ID ABX50975/c
XX ABX50975 standard; cDNA; 265 BP.
AC ABX50975;
XX
DT 25-FEB-2003 (first entry)
DE Bovine EST associated with lactation/muscle/fat deposition #904.
XX
XX Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
KW muscle deposition; fat deposition; genome mapping; gene identification;
KW gene analysis; cattle breeding.
XX
OS Bos Taurus.
PN US2002137160-A1.
XX
PD 26-SEP-2002.
XX
PF 26-OCT-2001; 2001US-00983965.
PR 17-DEC-1998; 98US-0113678P.
PR 15-DEC-1999; 99US-00465231.
XX
XX (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
XX
PI Byatt JC, Mathialagan N, Tao N, Warren WC;
XX WPI; 2003-102386/09.
XX
PT Purified nucleic acid molecules, useful for genome mapping, gene
PT identification and analysis, cattle breeding or preparation of constructs
PT for cattle gene expression and genetically improved cattle.
XX
PS Claim 2; SEQ ID NO 904; 38pp; English.
XX
CC The invention relates to a purified nucleic acid molecule associated with
CC lactation or muscle and fat deposition (designated LMFD), derived from
CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
CC nucleic acid molecule comprising any of 5912 nucleotide sequences,
CC appearing as ABX50072-ABX55983, or complements of them. Also included are
CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
CC acid linked to a promoter and a 3' non-translated sequence that
CC functions in the cell to cause termination of transcription and addition
CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
CC (2) determining a level or pattern of a molecule in a bovine cell or
CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
CC of the 5912 nucleic acid sequences or its complement or fragment) with a
CC complementary nucleic acid molecule obtained from the bovine cell or
CC tissue, where hybridisation between the marker nucleic acid and the
CC complementary nucleic acid permits the detection of the molecule; and (b)
CC detecting the level or pattern of the complementary nucleic acid, where
CC the detection of the complementary nucleic acid is predictive of the
CC level or pattern of the molecule. The LMFD nucleic acid is used for
CC determining a level or pattern of a molecule in a bovine cell or tissue.

CC It is useful for genome mapping, gene identification and analysis, cattle
CC breeding, preparation of constructs for use in cattle gene expression, or
CC for genetically improving cattle. The present sequence is one of the 5912
CC bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The present
CC sequence was not shown in the specification but was obtained in
CC electronic format from the USPTO web site:
CC seqdata.uspto.gov/sequence.html?DocID=20020137160
XX
SQ Sequence 265 BP; 67 A; 72 C; 67 G; 59 T; 0 U; 0 Other;
Query Match 72.7%; Score 16; DB 7; Length 265;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTTGTGCTTATCGGG 16
DB 217 CTTGTGCTTATCGGG 202
RESULT 9
ID ABL17664/c
XX ABL17664 standard; DNA; 23654 BP.
AC ABL17664;
XX
DT 26-MAR-2002 (first entry)
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 4465.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX
OS Drosophila melanogaster.
XX
PN W0200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
XX (PEKE) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions.
XX
PS Claim 1; SEQ ID NO 4465; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS57737-
CC ABBS70721). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 23654 BP; 6479 A; 5244 C; 5233 G; 6698 T; 0 U; 0 Other;
Query Match 68.2%; Score 15; DB 4; Length 23654;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 TTATCCGGCAAGAA 22

Db 20478 TTATCCGGGCAAGNA 20464

|||||

RESULT 10
ADB12176/c
ID ADB12176 standard; DNA; 438 BP.

XX AC ADB12176;

XX DT 20-NOV-2003 (first entry)

XX DE Alloicoccus otitis antigenic protein encoding DNA SEQ ID NO:6539.

XX KW Alloicoccus otitidis; antigenic protein; immunogenic; immunisation;
XX gene therapy; Gram-positive bacterium; infection; gene; ds.

XX OS Alloicoccus otitis.

XX PN WO2003048304-A2.

XX PD 12-JUN-2003.

XX PF 25-NOV-2002; 2002WO-US036123.

XX PR 29-NOV-2001; 2001US-0333777P.

XX PR 18-NOV-2002; 2002US-0426742P.

XX PA (AMHP) WYETH HOLDINGS CORP.

XX PI Fletcher LD, McMichael JC, Russell DP, Zagursky RJ;

XX WPI; 2003-505284/47.

XX P-PSDB; ADB12173.

XX PT New alloicoccus otitidis polynucleotides and polypeptides, useful for
PT treating and diagnosing diseases, drug screening assays and monitoring of
PT effects during drug clinical trials.

XX PS Claim 7; SEQ ID NO 6539; 1019pp; English.

XX CC The present invention describes an isolated polynucleotide (I) of
CC Alloicoccus otitidis genomic DNA, which encodes an antigenic protein.
CC Alloicoccus otitidis is a gram-positive bacterium. Also described: (1)
CC an isolated polypeptide that is encoded by the polynucleotide (I); (2) an
CC expression vector comprising the novel isolated polynucleotide (I), its
CC complement, degenerate variant or fragment; (3) a genetically engineered
CC host cell, transfected, transformed or infected with the vector of (2);
CC (4) an antibody specific for the polypeptide of (1); (5) an immunogenic
CC composition comprising the polypeptide, its complement, biological
CC equivalent or fragment, or the polynucleotide that is comprised in the
CC expression vector; (6) a pharmaceutical composition comprising the
CC polypeptide of (1) and a carrier; (7) a protein chip comprising an array
CC of the polypeptides of (1), their biological equivalent or fragment; (8)
CC immunising against Alloicoccus otitidis by administering to a host the
CC immunogenic composition; (9) detecting and/or identifying Alloicoccus
CC otitidis in the biological sample; (10) a kit comprising a container
CC containing the novel polynucleotide, its degenerate variant or fragment,
CC or the antibody of (4); and (11) producing a polypeptide by culturing the
CC genetically engineered host cell under conditions suitable to produce the
CC polypeptide from the culture. (I) can be used in gene therapy. The
CC polynucleotides, polypeptides, antibodies and compositions of the present
CC invention can be used for treating and diagnosing diseases, drug
CC screening assays and monitoring of effects during drug clinical trials.
CC The polynucleotides are useful for expressing and detecting Alloicoccus
CC otitidis. The present sequence encodes an Alloicoccus otitidis antigen
CC protein from the present invention.

XX SQ Sequence 438 BP; 119 A; 106 C; 108 G; 105 T; 0 U; 0 Other;

Query Match

63.6%; Score 14; DB 8; Length 438;

Best Local Similarity 100.0%; Pred. No. 93;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTGTGCTTATCCGG 15
| | | | | | | | | | | | | | | | | | | | |
Db 232 TTGTGCTTATCCGG 219

RESULT 11
ABK75795
ID ABK75795 standard; DNA; 717 BP.

XX AC ABK75795;

XX DT 13-AUG-2002 (first entry)

XX DE Bacillus licheniformis genomic sequence tag (GST) #3086.

XX KW Differential gene expression; genomic sequenced tag; GST;
XX altered culture condition; environmental stress;
XX physiological provocation; ds.

XX OS Bacillus licheniformis.

XX PN WO200229113-A2.

XX PD 11-APR-2002.

XX PF 05-OCT-2001; 2001WO-US031437.

XX PR 06-OCT-2000; 2000US-00680598.

XX PR 27-MAR-2001; 2001US-0279526P.

XX PA (NOVO) NOVOZYMES BIOTECH INC.

XX PI Berka R, Clausen IG;

XX WPI; 2002-416684/44.

XX PT Monitoring differential expression of several genes in first Bacillus
PT cell relative to expression of same genes in one or more second Bacillus
PT cells, by using substrate containing Bacillus genomic sequenced tag
PT array.

XX PS Claim 4; SEQ ID NO 3086; 200pp; English.

XX CC The invention describes a method of monitoring differential expression of
CC genes in a first Bacillus cell relative to expression of the genes in
CC other Bacillus cells, comprising hybridising labelled nucleic acid probes
CC isolated from Bacillus cells to a substrate containing array of Bacillus
CC genomic sequenced tags (GST), examining the array, and determining
CC relative gene expression by an observed hybridisation reporter signal of
CC a spot in the array. The method is useful for measuring the expression of
CC genes in a first Bacillus cell relative to expression of the same genes
CC in one or more second Bacillus cells. The method is useful for monitoring
CC global expression of several genes from a Bacillus cell, discovering new
CC genes, identifying possible functions of unknown open reading frames and
CC monitoring gene copy number, variation and stability. Monitoring changes
CC in expression of genes may be used to provide a representation of the way
CC in which Bacillus cells adapt to changes in culture conditions,
CC environmental stress or other physiological provocation. Extensive follow
CC -up characterisation is unnecessary, when one spot on an array equals one
CC gene or one open reading frame, since sequence information is available.
CC This sequence represents a genomic sequence tag (GST) used in the method
CC of the invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 717 BP; 189 A; 165 C; 175 G; 188 T; 0 U; 0 Other;

Query Match

63.6%; Score 14; DB 6; Length 717;

Best Local Similarity 100.0%; Pred. No. 92;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGCTTATCCGGCA 18
Db 373 TGCTTATCCGGCA 386

RESULT 12

AA91767
ID AAX91767 standard; DNA; 945 BP.

XX AC AAX91767;
XX DT 27-AUG-2003 (revised)
XX DT 20-MAR-2003 (revised)
XX DT 25-AUG-1999 (first entry)

XX DE Porphorymonas gingivalis protein PG78 encoding DNA.
XX KW Porphorymonas gingivalis; PG; periodontal disease; gingivitis; vaccine;
XX KW antigenic; ds.
XX OS Porphorymonas gingivalis.
XX PN WO9929870-A1.
XX PD 17-JUN-1999.

XX PF 10-DEC-1998; 98WO-AU001023.
XX PR 10-DEC-1997; 97AU-00000839.
XX PR 31-DEC-1997; 97AU-00001182.
XX PR 30-JAN-1998; 98AU-00001546.
XX PR 10-MAR-1998; 98AU-00002264.
XX PR 09-APR-1998; 98AU-00002911.
XX PR 23-APR-1998; 98AU-00003128.
XX PR 05-MAY-1998; 98AU-00003338.
XX PR 29-JUL-1998; 98AU-00004917.
XX PR 04-AUG-1998; 98AU-00005028.

XX PA (CSLC-) CSL LTD.
XX PI Ross BC, Barr IG, Patterson MA, Agius CT, Rothel LJ, Margetts MB;
XX PI Hocking DM, Webb EA;
XX PS WPI: 1999-385613/32.
XX PS P-PSDB; AAX34549.

XX PT Antigenic Porphorymonas gingivalis peptides for preventing gingivitis.
XX PS Claim 12; Page 253-254; 589pp; English.
XX CC AAX91536 to AAX91801 encode two hundred and sixty six antigenic
CC Porphorymonas gingivalis (PG) polypeptide sequences given in AAX34318 to
CC AAX34583. AAX91802 to AAX91989 represent PCR primers used in the
CC isolation of the PG polypeptides. The PG polypeptides have antibacterial
CC activity with a vaccine mechanism of action. The PG polypeptides can be
CC used as vaccines especially against Porphorymonas gingivalis. Probes can
CC be used to detect Porphorymonas gingivalis in standard hybridisation
CC assays. Porphorymonas gingivalis is involved in periodontal disease
CC especially gingivitis. (Updated on 20-MAR-2003 to correct PR field.)
XX SQ Sequence 945 BP; 207 A; 245 C; 226 G; 267 T; 0 U; 0 Other;
Query Match 63.6%; Score 14; DB 2; Length 945;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CTTATCCGGCAAG 20
Db 710 CTTATCCGGCAAG 723

RESULT 13

AA91633
ID AAX91633 standard; DNA; 987 BP.

XX AC AAX91633;
XX DT 27-AUG-2003 (revised)
XX DT 20-MAR-2003 (revised)
XX DT 25-AUG-1999 (first entry)

XX DE Porphorymonas gingivalis protein PG78 ORF encoding DNA.
XX KW Porphorymonas gingivalis; PG; periodontal disease; gingivitis; vaccine;
XX KW antigenic; ds.
XX OS Porphorymonas gingivalis.
XX PN WO9929870-A1.
XX PD 17-JUN-1999.

XX PF 10-DEC-1998; 98WO-AU001023.
XX PR 10-DEC-1997; 97AU-00000839.
XX PR 31-DEC-1997; 97AU-00001182.
XX PR 30-JAN-1998; 98AU-00001546.
XX PR 10-MAR-1998; 98AU-00002264.
XX PR 09-APR-1998; 98AU-00002911.
XX PR 23-APR-1998; 98AU-00003128.
XX PR 05-MAY-1998; 98AU-00003338.
XX PR 22-MAY-1998; 98AU-00003654.
XX PR 29-JUL-1998; 98AU-00004917.
XX PR 04-AUG-1998; 98AU-00005028.

XX PA (CSLC-) CSL LTD.
XX PI Ross BC, Barr IG, Patterson MA, Agius CT, Rothel LJ, Margetts MB;
XX PI Hocking DM, Webb EA;
XX PS WPI: 1999-385613/32.
XX PS P-PSDB; AAX34415.

XX PT Antigenic Porphorymonas gingivalis peptides for preventing gingivitis.
XX PS Claim 12; Page 162; 588pp; English.
XX CC AAX91536 to AAX91801 encode two hundred and sixty six antigenic
CC Porphorymonas gingivalis (PG) polypeptide sequences given in AAX34318 to
CC AAX34583. AAX91802 to AAX91989 represent PCR primers used in the
CC isolation of the PG polypeptides. The PG polypeptides have antibacterial
CC activity with a vaccine mechanism of action. The PG polypeptides can be
CC used as vaccines especially against Porphorymonas gingivalis. Probes can
CC be used to detect Porphorymonas gingivalis in standard hybridisation
CC assays. Porphorymonas gingivalis is involved in periodontal disease
CC especially gingivitis. (Updated on 20-MAR-2003 to correct PR field.)
XX SQ Sequence 987 BP; 215 A; 258 C; 239 G; 275 T; 0 U; 0 Other;
Query Match 63.6%; Score 14; DB 2; Length 987;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CTTATCCGGCAAG 20
Db 752 CTTATCCGGCAAG 765

RESULT 14

AAV80227/c
ID AAV80227 standard; DNA; 1262 BP.

```

XX AC AAV80227;
XX DT 02-MAR-1999 (first entry)
XX DE Maize globulin promoter sequence.
XX KW Maize; acyl-ACP thioesterase; enzyme; oleoyl-ACP thioesterase; OTE; PTE;
XX KW palmitoyl-ACP thioesterase; transgenic plant; oil; fatty acid; promoter;
XX KW regulatory element; transcriptional terminator; globulin; ss.
XX OS Zea mays.
XX PN WO9850569-A2.
XX PD 12-NOV-1998.
XX XX
XX PF 22-APR-1998; 98WO-US008097.
XX PR 05-MAY-1997; 97US-0045827P.
XX PA (DOWC ) DOW AGROSCIENCES LLC.
XX PI Rubin-Wilson B, Guo L, Skokut T, Young S, Folkerts O;
XX PI Armstrong K, Cowen NM;
XX DR WPI; 1999-034732/03.
XX XX
XX PT Composition comprising a promoter regulatory element, acyl-ACP
XX PT thioesterase coding sequence, and a terminator - useful for, e.g.
XX PT production of plant oil with an altered fatty acid content.
XX PS Claim 2; Page 142-144; 179pp; English.
XX CC The invention relates to genes encoding maize acyl-ACP thioesterase
XX CC enzymes. The enzymes especially, oleoyl-ACP thioesterase (OTE) and
XX CC palmitoyl-ACP thioesterase (PTE) can be used to create transgenic plants
XX CC having altered oil profiles. The invention provides a composition
XX CC comprising in a 5' to 3' direction: (i) a promoter regulatory element;
XX CC (ii) an acyl-ACP thioesterase encoding nucleic acid isolated from maize,
XX CC and (iii) a transcriptional terminator. The compositions and plant cell
XX CC of comprising the compositions can be used to produce plant oil having
XX CC altered levels of fatty acids. The present sequence represents the maize
XX CC globulin promoter sequence
XX SQ Sequence 1262 BP; 380 A; 288 C; 248 G; 346 T; 0 U; 0 Other;

Query Match 63.6%; Score 14; DB 2; Length 1262;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTGCTTATCGGGC 17
Db 1069 GTGCTTATCGGGC 1056

RESULT 15
ABA94959/c
ID ABA94959 standard; DNA; 1262 BP.
XX AC ABA94959;
XX DT 08-MAY-2002 (first entry)
XX DE Globulin seed specific promoter fragment.
XX KW Beta-ketoacyl-acyl carrier protein synthase II; KAS II; maize; soybean;
XX KW oil; fatty acid; transgenic; plant; globulin; promoter; ds.
XX OS Synthetic.
XX PN US6323395-B1.
XX XX

```

```

PD 27-NOV-2001.
XX XX
XX PF 16-DEC-1998; 98US-00212609.
XX PR 24-DEC-1997; 97US-0068784P.
XX PA (DOWC ) DOW AGROSCIENCES LLC.
XX PI Rubin-Wilson BC, Young SA, Folkerts O;
XX DR WPI; 2002-178575/23.
XX XX
XX PT New DNA construct useful as vector to transform plants, particularly
XX PT corn, with modified saturated fat content contains nucleic acid encoding
XX PT beta-ketoacyl-acyl carrier protein synthase II isolated from maize or
XX PT soybean.
XX PS Example 7; Col 83-84; 44pp; English.
XX CC The invention relates to genes encoding beta-ketoacyl-acyl carrier
XX CC protein synthase II (KAS II) isolated from maize or soybean tissues. The
XX CC saturate levels of oils found in plant cells can be altered by modifying
XX CC the expression and activity levels of KAS II within the cell. A DNA
XX CC construct comprising in the 5' to 3' direction, a promoter regulatory
XX CC element, a nucleic acid fragment encoding KAS II and a transcriptional
XX CC terminator can be used to modify the saturated fat content of transgenic
XX CC plants, particularly corn. The present sequence represents a globulin
XX CC seed specific promoter fragment used in the construction of
XX CC transformation vectors
XX SQ Sequence 1262 BP; 380 A; 288 C; 248 G; 346 T; 0 U; 0 Other;

Query Match 63.6%; Score 14; DB 6; Length 1262;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTGCTTATCGGGC 17
Db 1069 GTGCTTATCGGGC 1056

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Job time : 109.207 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 17:27:15 ; Search time 492.914 Seconds
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Searched: 3470272 seqs, 21671516995 residues

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Pred. No. is the number of results predicted by chance to have a

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and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	22	100.0	22	6	AX513219	AX513219 Sequence
2	22	100.0	22	6	AX513224	AX513224 Sequence
3	22	100.0	51	6	AX513217	AX513217 Sequence
4	22	100.0	51	6	AX513222	AX513222 Sequence
5	22	100.0	212	9	AF262303	AF262303 Homo sapi
6	22	100.0	260	9	AF224495	AF224495 Homo sapi
7	22	100.0	348	9	AF262299	AF262299 Homo sapi
8	22	100.0	406	9	AF262301	AF262301 Homo sapi
9	22	100.0	410	9	AF262302	AF262302 Homo sapi
10	22	100.0	436	9	AF262304	AF262304 Homo sapi
11	22	100.0	957	9	AF224496S1	AF224496 Homo sapi
12	22	100.0	1453	9	AF247360	AF247360 Homo sapi
13	22	100.0	2895	6	AX513212	AX513212 Sequence
14	22	100.0	2895	9	AF237380S1	AF237380 Homo sapi
15	22	100.0	177334	9	AC138069	AC138069 Homo sapi
16	22	100.0	197279	9	AC104439	AC104439 Homo sapi
17	22	100.0	220965	2	HSB312688	AJ312688 Homo sapi
18	21	95.5	1193	6	AR300122	AR300122 Sequence
19	21	95.5	1193	6	BD082061	BD082061 G-protein
20	18	81.8	31654	3	CEC32H11	282260 Caenorhabdi
21	17	77.3	1454	9	AF247359	AF247359 Homo sapi
22	16	72.7	45336	10	AL935309	AL935309 Mouse DNA
23	16	72.7	165837	2	AC101908	AC101908 Mus muscu
24	16	72.7	218358	2	AC145931	AC145931 Gallus ga
25	16	72.7	235349	2	AC109855	AC109855 Rattus no
26	15	68.2	4161	1	BSF133614	AJ133614 Bacillus
27	15	68.2	61421	2	AC103765	AC103765 Homo sapi
28	15	68.2	76854	3	AC003052	AC003052 Drosophil
29	15	68.2	83991	8	AP004965	AP004965 Lotus cor
30	15	68.2	86398	2	AC017785	AC017785 Drosophil
31	15	68.2	133974	2	AC108894	AC108894 Bos tauru
32	15	68.2	157533	2	AC133903	AC133903 Mus muscu
33	15	68.2	158113	4	AC136966	AC136966 Bos tauru
34	15	68.2	166537	2	AC131916	AC131916 Mus muscu
35	15	68.2	167201	3	AC092397	AC092397 Drosophil
36	15	68.2	176486	8	AP003768	AP003768 Oryza sat
37	15	68.2	188654	2	AC136320	AC136320 Mus muscu
38	15	68.2	197461	2	AC134814	AC134814 Rattus no
39	15	68.2	221649	2	AC147442	AC147442 Gallus ga
40	15	68.2	232049	2	AC127108	AC127108 Rattus no
41	15	68.2	235572	2	AC134470	AC134470 Mus muscu
42	15	68.2	246237	3	CEY39B6A	AL132948 Caenorhab
43	15	68.2	260139	3	AE003614	AE003614 Drosophil
44	15	68.2	305961	1	AE016937	AE016937 Bacteroid
45	15	68.2	339977	2	AC109846	AC109846 Rattus no

ALIGNMENTS

RESULT 1
AX513219
LOCUS AX513219 22 bp DNA linear PAT 03-OCT-2002
DEFINITION Sequence 18 from Patent WO02062848.
ACCESSION AX513219
VERSION AX513219.1 GI:23504282
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Rothenberg, M.E. and Zimmerman, N.
TITLE Regulation of cc chemokine receptor 3 (ccr3) expression
JOURNAL Patent: WO 02062848-A 18 15-AUG-2002;

CHILDREN'S HOSPITAL MEDICAL CENTER (US)

FEATURES
source

Location/Qualifiers
1. .22
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 22; DB 6; Length 22;

Best Local Similarity 100.0%; Pred. No. 0.049; Mismatches 0; Indels 0; Gaps 0;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGTGCTTATCCGGCAAGAA 22

Db 1 CTTGTGCTTATCCGGCAAGAA 22

RESULT 2

AX513224
LOCUS AX513224 22 bp RNA linear PAT 03-OCT-2002

DEFINITION Sequence 23 from Patent WO02062848.

ACCESSION AX513224

VERSION AX513224.1 GI:23504287

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE

AUTHORS Rothenberg,M.E. and Zimmerman,N.

TITLE Regulation-of-cc-chemokine receptor 3 (ccr3) expression

JOURNAL Patent: WO 02062848-A 23 15-AUG-2002;

CHILDREN'S HOSPITAL MEDICAL CENTER (US)

FEATURES

source

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Best Local Similarity 100.0%; Pred. No. 0.048; Mismatches 0; Indels 0; Gaps 0;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGTGCTTATCCGGCAAGAA 22

Db 1 CTTGTGCTTATCCGGCAAGAA 22

RESULT 3

AX513217
LOCUS AX513217 51 bp DNA linear PAT 03-OCT-2002

DEFINITION Sequence 16 from Patent WO02062848.

ACCESSION AX513217

VERSION AX513217.1 GI:23504280

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE

AUTHORS Rothenberg,M.E. and Zimmerman,N.

TITLE Regulation of cc chemokine receptor 3 (ccr3) expression

JOURNAL Patent: WO 02062848-A 16 15-AUG-2002;

CHILDREN'S HOSPITAL MEDICAL CENTER (US)

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source

1. .51

/organism="Homo sapiens"

/mol_type="unassigned DNA"

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ORIGIN

Query Match 100.0%; Score 22; DB 6; Length 51;

Best Local Similarity 100.0%; Pred. No. 0.043;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGTGCTTATCCGGCAAGAA 22

Db 16 CTTGTGCTTATCCGGCAAGAA 37

RESULT 4

AX513222
LOCUS AX513222 51 bp RNA linear PAT 03-OCT-2002

DEFINITION Sequence 21 from Patent WO02062848.

ACCESSION AX513222

VERSION AX513222.1 GI:23504285

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE

AUTHORS Rothenberg,M.E. and Zimmerman,N.

TITLE Regulation of cc chemokine receptor 3 (ccr3) expression

JOURNAL Patent: WO 02062848-A 21 15-AUG-2002;

CHILDREN'S HOSPITAL MEDICAL CENTER (US)

FEATURES

source

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Best Local Similarity 100.0%; Pred. No. 0.043; Mismatches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGTGCTTATCCGGCAAGAA 22

Db 16 CTTGTGCTTATCCGGCAAGAA 37

RESULT 5

AF262303
LOCUS AF262303 212 bp mRNA linear PRI 26-JUN-2002

DEFINITION Homo sapiens clone 6 CC chemokine receptor 3 (CCR3) mRNA, partial

CDs.

ACCESSION AF262303

VERSION AF262303.1 GI:19171648

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 212)

Vijh,S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and

Michael,N.L.

TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence

for a Rare TATA-less Promoter Structure Conserved between

Drosophila and Humans

JOURNAL Genomics 80 (1), 86-95 (2002)

MEDLINE 22074933

PUBMED 12079287

REFERENCE 2 (bases 1 to 212)

AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.

TITLE Direct Submission

JOURNAL Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis,

Walter Reed Army Institute of Research, 1600 E. Gude Drive,

Rockville, MD 20850, USA

FEATURES

source

1. .212

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1. .>212
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CD8 lymphocytes, microglia, dendritic cells, and
monocytes"
/codon_start=1
/product="CC chemokine receptor 3"
/protein_id="AAL85632.1"
/db_xref="GI:19171649"
/translation="MTISLDIVETFGTTSYDDVG"

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Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGTGCTTATCCGGCAAGAA 22
DB 12 CTTGTGCTTATCCGGCAAGAA 33

RESULT 6
LOCUS AF224495 260 bp mRNA linear PRI 02-MAY-2001
DEFINITION Homo sapiens CC chemokine receptor 3 (CCR3) mRNA, partial cds.
ACCESSION AF224495
VERSION AF224495.1 GI:13924481
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 260)
AUTHORS Scotet,E.J.
TITLE CCR3 expression is associated with chromatin remodeling in Th2
cells
JOURNAL Unpublished
2 (bases 1 to 260)
AUTHORS Scotet,E.J.
DIRECT SUBMISSION
TITLE Direct Submission
JOURNAL Submitted (13-JAN-2000) Basel Institute for Immunology, 487
Grenzacherstrasse, Basel CH-4005, Switzerland
FEATURES
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/db_xref="GI:13924482"
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gene
CDS

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Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGTGCTTATCCGGCAAGAA 22
DB 13 CTTGTGCTTATCCGGCAAGAA 34

RESULT 7
LOCUS AF262299 348 bp mRNA linear PRI 26-JUN-2002
DEFINITION Homo sapiens clone 1 CC chemokine receptor 3 (CCR3) mRNA, partial
cds.
ACCESSION AF262299
VERSION AF262299.1 GI:19171640
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 348)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Iman,Z., Ehrenberg,P.K. and
Michael,N.L.
TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence
for a Rare TATA-less Promoter Structure Conserved between
Drosophila-and-Humans
JOURNAL Genomics 80 (1), 86-95 (2002)
MEDLINE 22074933
PUBMED 12073287
2 (bases 1 to 348)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
DIRECT SUBMISSION
TITLE Direct Submission
JOURNAL Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis,
Walter Reed Army Institute of Research, 1600 E. Gude Drive,
Rockville, MD 20850, USA
FEATURES
location/Qualifiers
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120..>348
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CD8 lymphocytes, microglia, dendritic cells, and
monocytes"
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/protein_id="AAL85628.1"
/db_xref="GI:19171641"
/translation="MTISLDIVETFGTTSYDDVGLLCEKADTRALMAQFVPPLYSLV
FTVGLLGNVVVVMLIKYRRLRIMNIIYLNL"

gene
CDS

Query Match 100.0%; Score 22; DB 9; Length 348;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGTGCTTATCCGGCAAGAA 22
DB 42 CTTGTGCTTATCCGGCAAGAA 63

RESULT 8
LOCUS AF262301 406 bp mRNA linear PRI 26-JUN-2002
DEFINITION Homo sapiens clone 4 CC chemokine receptor 3 (CCR3) mRNA, partial
cds.
ACCESSION AF262301
VERSION AF262301.1 GI:19171644
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 406)
 Vajh.S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and Michael,N.L.
 Transcription Regulation of Human Chemokine Receptor CCR3: Evidence for a Rare TATA-less Promoter Structure Conserved between Drosophila and Humans
 Genomics 80 (1), 86-95 (2002)
 22074933
 12079287
 REFERENCE 2 (bases 1 to 406)
 Vajh.S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
 Direct Submission
 TITLS Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis, Walter Reed Army Institute of Research, 1600 E. Gude Drive, Rockville, MD 20850, USA
 JOURNAL Location/Qualifiers
 FEATURES
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 /organism="Homo sapiens"
 /mol_type="mRNA"
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 /chromosome="3"
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 180. .>406
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 /product="CC chemokine receptor 3"
 /protein_id="AAL85630.1"
 /db_xref="GI:19171645"
 /translation="MTSLDTVETFGTTSYDDVGLLCEKADTRALMAQFVPLYSLV
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 Best Local Similarity 100.0%; Pred. No. 0.034;
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 QY 1 CTTGTGCTTATCCGGCAAGAA 22
 |||||
 Db 13 CTTGTGCTTATCCGGCAAGAA 34
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 AF262302
 LOCUS Homo sapiens clone 5 CC chemokine receptor 3 (CCR3) mRNA, partial cds.
 DEFINITION
 ACCESSION AF262302
 VERSION AF262302.1 GI:19171646
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 410)
 Vajh.S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and Michael,N.L.
 Transcription Regulation of Human Chemokine Receptor CCR3: Evidence for a Rare TATA-less Promoter Structure Conserved between Drosophila and Humans
 Genomics 80 (1), 86-95 (2002)
 22074933
 12079287
 REFERENCE 2 (bases 1 to 410)
 Vajh.S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
 Direct Submission
 TITLS Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis, Walter Reed Army Institute of Research, 1600 E. Gude Drive, Rockville, MD 20850, USA
 JOURNAL Location/Qualifiers
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Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis, Walter Reed Army Institute of Research, 1600 E. Gude Drive, Rockville, MD 20850, USA
 JOURNAL Location/Qualifiers
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 /db_xref="GI:19171647"
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 Best Local Similarity 100.0%; Pred. No. 0.033;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTTGTGCTTATCCGGCAAGAA 22
 |||||
 Db 13 CTTGTGCTTATCCGGCAAGAA 34
 RESULT 10
 AF262304
 LOCUS Homo sapiens clone 7 CC chemokine receptor 3-like mRNA, partial sequence, alternatively spliced.
 DEFINITION
 ACCESSION AF262304
 VERSION AF262304.1 GI:19171650
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 436)
 Vajh.S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and Michael,N.L.
 Transcription Regulation of Human Chemokine Receptor CCR3: Evidence for a Rare TATA-less Promoter Structure Conserved between Drosophila and Humans
 Genomics 80 (1), 86-95 (2002)
 22074933
 12079287
 REFERENCE 2 (bases 1 to 436)
 Vajh.S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
 Direct Submission
 TITLS Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis, Walter Reed Army Institute of Research, 1600 E. Gude Drive, Rockville, MD 20850, USA
 JOURNAL Location/Qualifiers
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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGTGCTTATCCGGGCAAGAA 22
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Db 12 CTTGTGCTTATCCGGGCAAGAA 33

RESULT 11
AF224496S1 957 bp DNA linear PRI 02-MAY-2001
DEFINITION Homo sapiens CC chemokine receptor 3 (CCR3) gene, exon 1.
ACCESSION AF224496
VERSION AF224496.1 GI:13924485
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 957)
AUTHORS Scotet,E.J.
TITLE CCR3 expression is associated with chromatin remodeling in Th2
cells
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 957)
AUTHORS Scotet,E.J.
TITLE Direct Submission
JOURNAL Submitted (13-JAN-2000) Basel Institute for Immunology, 487
Grenzacherstrasse, Basel CH-4005, Switzerland
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source
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Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGTGCTTATCCGGGCAAGAA 22
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Db 310 CTTGTGCTTATCCGGGCAAGAA 331

RESULT 12
AF247360 1453 bp DNA linear PRI 26-JUN-2002
DEFINITION Homo sapiens CC chemokine receptor 3 (CCR3) gene, promoter region
and partial sequence.
ACCESSION AF247360
VERSION AF247360.1 GI:19110541
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1453)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and
Michael,N.L.
TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence
for a Rare TATA-less Promoter Structure Conserved between
Drosophila and Humans

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Genomics 80 (1), 86-95 (2002)
JOURNAL MEDLINE 22074933
PUBMED 12079287
REFERENCE 2 (bases 1 to 1453)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
TITLE Direct Submission
JOURNAL Submitted (21-MAR-2000) Dept. of Mol. Diag. and Pathogenesis, U.S.
Military HIV Research Program, 1600 E. Gude Drive, Rockville, MD
20850, USA
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755
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822..1163
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Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGTGCTTATCCGGGCAAGAA 22
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Db 1097 CTTGTGCTTATCCGGGCAAGAA 1118

RESULT 13
AX513212 2895 bp DNA linear PAT 03-OCT-2002
LOCUS AX513212
DEFINITION Sequence 11 from Patent WO2062848.
ACCESSION AX513212
VERSION AX513212.1 GI:23504275
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Rothenberg,M.E. and Zimmerman,N.
TITLE Regulation of cc chemokine receptor 3 (ccr3) expression
JOURNAL Patent: WO 02062848-A 11 15-AUG-2002;
CHILDREN'S HOSPITAL MEDICAL CENTER (US)
FEATURES
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Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGTGCTTATCCGGGCAAGAA 22
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Db 1576 CTTGTGCTTATCCGGGCAAGAA 1597

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RESULT 14
LOCUS AF237380S1
DEFINITION Homo sapiens CCR3 gene, promoter and exon 1.
ACCESSION AF237380
VERSION AF237380.1 GI:10643652
KEYWORDS
SEGMENT
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Zimmermann, N., Daugherty, B.L., Kavanaugh, J.L., El-Awar, F.Y.,
Moulton, E.A. and Rotherberg, M.E.
TITLE Analysis of the CC chemokine receptor 3 gene reveals a complex 5'
exon organization, a functional role for untranslated exon 1, and a
broadly active promoter with eosinophil-selective elements
JOURNAL Blood 96 (7), 2346-2354 (2000)
MEDLINE 20458773
PUBMED 11001881
REFERENCE
AUTHORS 2 (bases 1 to 2895)
Daugherty, B.L.
Direct Submission
TITLE Submitted (22-FEB-2000) Immunology & Rheumatology, Merck Research
Laboratories, 126 East Lincoln Avenue, Rahway, NJ 07065, USA
JOURNAL
FEATURES
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Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGTCCTATCCGGCAAGAA 22
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Db 1576 CTTGTCCTATCCGGCAAGAA 1597

RESULT 15
LOCUS AC138069
DEFINITION Homo sapiens chromosome 3 clone RP13-54612, complete sequence.
ACCESSION AC138069
VERSION AC138069.3 GI:28416170
KEYWORDS HTG.
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 177334)
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
Saenphimmachak, C., Buckley, D., Kibukawa, M., Raymond, C. and

```

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Haugen, E.D.
Direct Submission
Unpublished
2 (bases 1 to 177334)
Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.
Direct Submission
Submitted (12-DEC-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
3 (bases 1 to 177334)
Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.
Direct Submission
Submitted (10-JAN-2003) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
4 (bases 1 to 177334)
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
Saenphimmachak, C., Buckley, D., Kibukawa, M., Raymond, C. and
Haugen, E.D.
Direct Submission
Submitted (19-FEB-2003) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
On Feb 19, 2003 this sequence version replaced gi:27573398.
COMMENT
----- Genome Center
Center: University of Washington Genome Center
Center Code: UWGC
Web site: http://www.genome.washington.edu
Contact: uwgchtgs@u.washington.edu
----- Project Information
Center project name: chr-3
Center clone name: RP13-54612 (bc0820)
----- Summary Statistics
Sequencing vector: plasmid; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 177210 bases at least Q40
Consensus quality: 177313 bases at least Q30
Consensus quality: 177334 bases at least Q20
Insert size: 177334; sum-of-contigs
Quality coverage: 9.3x in Q20 bases; sum-of-contigs
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Overlapping Sequences:
5': RP11-793E15 (UWGC:bc0564) AC104439, 95469-bp overlap
3': U95626, 42710-bp overlap
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Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
Genbank flat file format but are available as part
of this entry's ASN.1 file.
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This sequence was finished as follows unless otherwise noted:
all regions were either double-stranded or sequenced with an
alternate chemistry or covered by high quality data (i.e., Phred
quality >= 30); an attempt was made to resolve all sequencing
problems, such as compressions and repeats; all regions were
covered by at least one plasmid subclone or more than one M13
subclone; and the assembly was confirmed by restriction digest.
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Sequence Validation:
This sequence has been validated by Multiple Complete Digest
fingerprinting. Comparison of the experimentally derived digest
fragments with sequence-predicted fragments is given below.
The electronically-digested sequence consists of both insert and
vector, in order to accurately represent the entire circular BAC.
Small fragments below a variable cutoff (approximately 400-800 bp)
are not resolved in the fingerprint and hence do not appear
in the table. There are no significant remaining discrepancies
between the experimental and predicted values. Uniquely ordered
fragments are separated by dashed lines.
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HindIII
EcoRI
BgIII

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Query Match 100.0%; Score 22; DB 9; Length 177334;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGTGCTTATCCGGCAAGAA 22

Db 65708 CTTGTGCTTATCCGGCAAGAA 65729

Search completed: August 2, 2004, 19:07:55
Job time : 495.914 secs

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Result No.	Query $\frac{q}{Q}$			DB	ID	Description
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4	16	72.7	741	28	CC146471	CC146471 ZMMEBD000

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        non-activated adult donors. Library is oligo-dT primed
        and directionally cloned (EcoRV site is destroyed upon
        cloning). Average insert size 1.7 kb, insert size range
        1.2-3.3 kb. Library is normalized and enriched for
        full-length clones and was constructed by C. Gruber
        (Invitrogen). Research Genetics tracking code 027. Note:
        this is a NIH_MGC Library."

ORIGIN
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RESULT 2
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LOCUS CB390728 584 bp mRNA linear EST 15-MAY-2003
DEFINITION OSTF139F9_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION CB390728
VERSION CB390728.1 GI:30732438
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
REFERENCE 1 (bases 1 to 584)
AUTHORS Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M.,
Armstrong,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T.,
Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V.,
Tollas,P.P., Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
Doucette-Stamm,L., Hill,D.E. and Vidal,M.
C. elegans ORFeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
JOURNAL Nat. Genet. (2003) In press
COMMENT Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project ; Contact david_hilledeci.harvard.edu or
marc_vidal@dfci.harvard.edu
POLYA=NO.
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        /mol_type="mRNA"
        /strain="N2"
        /db_xref="taxon:6239"
        /sex="Hermaphrodite and male"
        /tissue_type="whole animal"
        /dev_stage="mixed stage"
        /clone_lib="AD-wrmcDNA"

/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"

ORIGIN
  Query Match 81.8%; Score 18; DB 14; Length 584;
  Best Local Similarity 100.0%; Pred. No. 5.5;
  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGTGCTTATCCGGGCAAG 20
    |||||
Db 233 TGTGCTTATCCGGGCAAG 250

RESULT 3
CB306183
LOCUS CB306183 690 bp DNA linear GSS 26-SEP-2003
DEFINITION tigr-gss-dog-17000360539649 Dog Library Canis familiaris genomic,
genomic survey sequence.
ACCESSION CB306183
VERSION CB306183.1 GI:36100308
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
REFERENCE 1 (bases 1 to 690)
AUTHORS Kirkness,E.F., Batna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
JOURNAL MEDLINE 22875432
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
Location/Qualifiers
  1..690
    /organism="Canis familiaris"
    /mol_type="genomic DNA"
    /strain="Standard Poodle"
    /db_xref="taxon:9615"
    /clone_lib="Dog Library"
    /note="Site 1: BstXI; Libraries were prepared from
    peripheral blood"

ORIGIN
  Query Match 77.3%; Score 17; DB 29; Length 690;
  Best Local Similarity 100.0%; Pred. No. 21;
  Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTGCTTATCCGGGCAAG 20
    |||||
Db 262 GTGCTTATCCGGGCAAG 278

RESULT 4
CC146471/c
LOCUS CC146471 741 bp DNA linear GSS 24-JUN-2003
DEFINITION ZMMBBB0008F04.f ZMMBBB Zea mays subsp. mays genomic clone
ACCESSION CC146471
VERSION CC146471.1 GI:30091664
KEYWORDS GSS.
Ze mays subsp. mays (maize)

```

ORGANISM Zea mays subsp. mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 741)
Yu, Y., Kim, H.R., Hatfield, J., Soderlund, C., Bharti, A.K., Messing, J., and Wing, R.
Sequencing of the maize genome
Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 440A, P.O. Box 210088, Tucson, AZ 85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: <http://genome.arizona.edu>
PCR Primers
FORWARD: T7
BACKWARD: M13r
Plate: 0008 row: F column: 04
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1. 741
/organism="Zea mays subsp. mays"
/mol_type="genomic DNA"
/cultivar="B73"
/sub_species="mays"
/db_xref="taxon:4578"
/clone="ZMMBB0008F04"
/lab_host="DH10B"
/clone_lib="ZMMBBb"
/note="Vector: pBeloBAC11; Site 1: HindIII; Site 2: HindIII; Zea mays L. ssp. mays"

ORIGIN
Query Match 72.7%; Score 16; DB 28; Length 741;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGCTTATCCGGGCAAG 20
|||||
Db 382 TGCTTATCCGGGCAAG 367
|||||

RESULT 5
CG810851
LOCUS
CG810851
DEFINITION .FSAL36TR LargeInsertGenomicLibrary Fusarium virguliforme genomic clone KMV3F4, genomic survey sequence.
ACCESSION
CG810851
VERSION
GSS.
KEYWORDS
Fusarium virguliforme
SOURCE
Fusarium virguliforme
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocerales; Nectriaceae; Nectria.
1 (bases 1 to 779)
Lightfoot, D.A. and Town, C.D.
Meksem, K., Ishihara, H., Koo, H., Shultz, J., Ali, S., Iqbal, J., End sequencing of BACs from a fingerprint physical map of the causative agent of soybean sudden death syndrome, *Fusarium virguliforme*
Unpublished (2003)
Contact: Chris Town and K. Meksem
The Center of Excellence in Soybean Research, Teaching and Outreach, Southern Illinois University at Carbondale and Plant Genomics, The Institute for Genomic Research
Room 176, Ag Building, Mail Code 4415, Carbondale, IL 62901-4415, USA and 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 618 453 3103 and 301-838-3523
Fax: 618 453-7457 and 301-838-0208

ORGANISM Zea mays subsp. mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 741)
Yu, Y., Kim, H.R., Hatfield, J., Soderlund, C., Bharti, A.K., Messing, J., and Wing, R.
Sequencing of the maize genome
Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 440A, P.O. Box 210088, Tucson, AZ 85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: <http://genome.arizona.edu>
PCR Primers
FORWARD: T7
BACKWARD: M13r
Plate: 0008 row: F column: 04
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1. 741
/organism="Zea mays subsp. mays"
/mol_type="genomic DNA"
/cultivar="B73"
/sub_species="mays"
/db_xref="taxon:4578"
/clone="ZMMBB0008F04"
/lab_host="DH10B"
/clone_lib="ZMMBBb"
/note="Vector: pBeloBAC11; Site 1: HindIII; Site 2: HindIII; Zea mays L. ssp. mays"

ORIGIN
Query Match 72.7%; Score 16; DB 28; Length 741;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGCTTATCCGGGCAAG 20
|||||
Db 382 TGCTTATCCGGGCAAG 367
|||||

RESULT 5
CG810851
LOCUS
CG810851
DEFINITION .FSAL36TR LargeInsertGenomicLibrary Fusarium virguliforme genomic clone KMV3F4, genomic survey sequence.
ACCESSION
CG810851
VERSION
GSS.
KEYWORDS
Fusarium virguliforme
SOURCE
Fusarium virguliforme
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocerales; Nectriaceae; Nectria.
1 (bases 1 to 779)
Lightfoot, D.A. and Town, C.D.
Meksem, K., Ishihara, H., Koo, H., Shultz, J., Ali, S., Iqbal, J., End sequencing of BACs from a fingerprint physical map of the causative agent of soybean sudden death syndrome, *Fusarium virguliforme*
Unpublished (2003)
Contact: Chris Town and K. Meksem
The Center of Excellence in Soybean Research, Teaching and Outreach, Southern Illinois University at Carbondale and Plant Genomics, The Institute for Genomic Research
Room 176, Ag Building, Mail Code 4415, Carbondale, IL 62901-4415, USA and 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 618 453 3103 and 301-838-3523
Fax: 618 453-7457 and 301-838-0208

Email: meksem@siu.edu; cdtown@tigr.org (URL: <http://Fusariumvirguliforme.siu.edu>)
Seq primer: CAGGAACAGCATGACG
Class: BAC ends.
Location/Qualifiers
1. 779
/organism="Fusarium virguliforme"
/mol_type="genomic DNA"
/cultivar="Monticello"
/db_xref="taxon:232082"
/clone="KMV3F4"
/clone_lib="LargeInsertGenomicLibrary"
/note="Organ: Hyphae; Vector: PINDIGOBAC5; A single spore derived culture was used. Hyphae were grown in an incubator for four days. Nuclei were isolated and embedded in agarose, restriction digested with Hind III. Large size DNA fragments were ligated in vector PINDIGOBAC5 and electro-transformed into DH10B cells."

ORIGIN
Query Match 72.7%; Score 16; DB 29; Length 779;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GCTTATCCGGGCAAGA 21
|||||
Db 645 GCTTATCCGGGCAAGA 660
|||||

RESULT 6
BB482778/c
LOCUS
BB482778
DEFINITION musculus cDNA clone D430015020 3', similar to U24655 Rattus norvegicus Lnk4 mRNA, mRNA sequence.
ACCESSION
BB482778.1 GI:9400387
VERSION
EST.
KEYWORDS
Mus musculus (house mouse)
SOURCE
Mus musculus
ORGANISM
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 191)
Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, F., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomimaga, N., Toya, T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Konno, H., et al.)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-resgsc.riken.go.jp,
<http://genome.gsc.riken.go.jp/>
URL: <http://genome.gsc.riken.go.jp/>
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermosensitization and thermoactivation of thermostable enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Kitsuai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,

Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp/>) for further details.

FEATURES
source
1. 191
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="D430015020"
/tissue_type="lung"
/dev_stage="13 days embryo"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 13 days embryo lung"
/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'
GAGAGAGAGCGCGCAACTCGAGTGTGTTTTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'
GAGAGAGATTCGAGTAAATTAATATCCCGCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified paluescript KS(+) after bulk excision from lambda FLC I."

ORIGIN

Query Match 68.2%; Score 15; DB 10; Length 191;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTGCTTATCGGCA 18

Db 37 GTGCTTATCGGCA 23

RESULT 7

BF153648/c
LOCUS
DEFINITION
BF153648 196 bp mRNA linear EST 11-SEP-2002
033A04 Mature tuber lambda ZAP Solanum tuberosum cDNA 5', mRNA
sequence.

ACCESSION BF153648

VERSION BF153648.1 GI:11035588

KEYWORDS EST.

SOURCE Solanum tuberosum (potato)

ORGANISM Solanum tuberosum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.

1 (bases 1 to 196)

Crookshanks, M., Emmersen, J., Welinder, K.G. and Nielsen, K.L.
The potato tuber transcriptome: analysis of 5077 expressed sequence tags

JOURNAL FEBS Lett. 506 (2), 123-126 (2001)

MEDLINE 21475600

PUBMED 11591384

COMMENT Contact: Karen G. Welinder

Institut for Biotechnology

Aalborg Universitet

Sohngaardsholmsvej 49, 9000 Aalborg, Denmark

Tel: +45 96358467

Fax: +45 98141808

Email: kgw@bio.auc.dk

High quality sequence stop: 196
POLYA=No.

FEATURES
source

1. 196
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Field grown Kuras"
/db_xref="taxon:4113"
/tissue_type="Tuber"
/clone_lib="Mature tuber lambda ZAP"
/note="Vector: Lambda ZAP"

ORIGIN

Query Match 68.2%; Score 15; DB 10; Length 196;

Best Local Similarity 100.0%; Pred. No. 2.7e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGTGCTTATCGG 15

Db 151 CTTGTGCTTATCGG 137

RESULT 8

BF1702619

LOCUS

DEFINITION

BF1702619 283 bp mRNA linear EST 18-SEP-2001

fr38n10.x1 zebrafish adult brain Danio rerio cDNA clone

IMAGE:4955779 3' similar to TR:035274 O35274 SPINOPHILIN.1; mRNA

sequence.

ACCESSION BF1702619

VERSION BF1702619.1 GI:15665248

KEYWORDS EST.

SOURCE Danio rerio (zebrafish)

ORGANISM Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 283)

Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M.,

Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,

Underwood, K., Stepcevic, M., Theising, B., Allen, M., Bowers, Y.,

Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,

Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,

Waterston, R. and Wilson, R.

WashU Zebrafish EST Project 1998

Unpublished (1998)

Contact: Stephen L. Johnson

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63109, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: zbratfish@watson.wustl.edu

cDNA Library Preparation: John Ngai. cDNA Library Arrayed by:

Matthew Clark. DNA Sequencing by: Washington University Genome

Sequencing Center Clone distribution: Genome Systems, St. Louis,

Missouri (web address: www.genomesystems.com) (email contact:

info@genomesystems.com) and Research Genetics, Huntsville, Alabama

(web address: www.resgen.com) (email contact: info@resgen.com) and

Ressourcentzentrum Primardatenbank, Berlin, Germany (web address:

www.rzpd.de)

Trace considered overall poor quality

Possible reversed clone: polyT not found

Seq primer: T7 from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1. 283

/organism="Danio rerio"

/mol_type="mRNA"

/db_xref="taxon:7955"

/clone="IMAGE:4955779"

/sex="mixed male and female"

/tissue_type="brain"

/dev_stage="adult"

/lab_host="E. coli DH10B"

FEATURES
source

1. 283
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:4955779"
/sex="mixed male and female"
/tissue_type="brain"
/dev_stage="adult"
/lab_host="E. coli DH10B"


```

/clone.lib="zebrafish adult brain"
/note=Vector: pZiPFOX; Site 1: NotI; Site 2: SalI;
Original library was constructed in lambdaZiPFOX. Mass
excision of the cDNA library was performed to yield
pZiPFOX plasmids. Insert check was done in original
library."

ORIGIN
Query Match      68.2%; Score 15; DB 12; Length 283;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TCGTTATCCGGGCAA 19
|||||
Db 229 TCGTTATCCGGGCAA 243

RESULT 9
BU097383/c
LOCUS tca-1868 tca Trypanosoma carassii cDNA clone 1012 5', mRNA
DEFINITION
ACCESSION BU097383
VERSION BU097383.1 GI:25125107
KEYWORDS EST.
SOURCE Trypanosoma carassii
ORGANISM Trypanosoma carassii
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE 1 (bases 1 to 327)
AUTHORS Aguero, F., Campo, V., Cremona, L., Jager, A., Di Noia, J.M.,
Overath, P., Sanchez, D.O. and Frasch, A.C.
TITLE Gene discovery in the freshwater fish parasite Trypanosoma
carassii: identification of trans-sialidase-like and mucin-like
genes
JOURNAL Infect. Immun. 70 (12), 7140-7144 (2002)
COMMENT Contact: Sanchez DO
Genomics and Bioinformatics
Instituto de Investigaciones Bioteologicas
Av. Gral Paz S/N, INII, Edificio 24, B 1650 KNA, San Martin, Buenos
Aires, Argentina.
Tel: (54-11) 4580/7255/7
Fax: (54-11) 4752-9639
Email: dsanchez@lib.unsam.edu.ar
Sequences were basecalled with phred and vector was masked with
crossmatch (see http://www.phrap.org). Sequences were then trimmed
from both ends to remove low quality bases and masked vector.
Plate: 10 row: 1 column: 2
Seq primer: T7.
FEATURES
Location/Qualifiers
source
1..327
/organism="Trypanosoma carassii"
/mol_type="mRNA"
/db_xref="taxon:38249"
/clone="1012"
/dev_stages="blood trypomastigote"
/lab_host="Goldfish (Carassius auratus)"
/clone.lib="tca"
/note=Vector: pSport1; Blood trypomastigotes were
obtained from goldfish and cultured as described (Overath
et al. Parasitol Res (1998) 84:1343) before obtaining total
RNA using TRIzol. cDNA library construction was made from
polyA+ mRNA using a poly-dT oligonucleotide as primer. The
cDNAs were cloned in a oriented manner using a commercial
kit (SuperScript Plasmid System for cDNA Synthesis and
Plasmid Cloning, Life Technologies)."

ORIGIN
Query Match      68.2%; Score 15; DB 13; Length 327;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TCGTTATCCGGGCAA 19
|||||
Db 229 TCGTTATCCGGGCAA 243

/clone.lib="zebrafish adult brain"
/note=Vector: pZiPFOX; Site 1: NotI; Site 2: SalI;
Original library was constructed in lambdaZiPFOX. Mass
excision of the cDNA library was performed to yield
pZiPFOX plasmids. Insert check was done in original
library."

ORIGIN
Query Match      68.2%; Score 15; DB 12; Length 283;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TCGTTATCCGGGCAA 19
|||||
Db 229 TCGTTATCCGGGCAA 243

RESULT 9
BU097383/c
LOCUS tca-1868 tca Trypanosoma carassii cDNA clone 1012 5', mRNA
DEFINITION
ACCESSION BU097383
VERSION BU097383.1 GI:25125107
KEYWORDS EST.
SOURCE Trypanosoma carassii
ORGANISM Trypanosoma carassii
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE 1 (bases 1 to 327)
AUTHORS Aguero, F., Campo, V., Cremona, L., Jager, A., Di Noia, J.M.,
Overath, P., Sanchez, D.O. and Frasch, A.C.
TITLE Gene discovery in the freshwater fish parasite Trypanosoma
carassii: identification of trans-sialidase-like and mucin-like
genes
JOURNAL Infect. Immun. 70 (12), 7140-7144 (2002)
COMMENT Contact: Sanchez DO
Genomics and Bioinformatics
Instituto de Investigaciones Bioteologicas
Av. Gral Paz S/N, INII, Edificio 24, B 1650 KNA, San Martin, Buenos
Aires, Argentina.
Tel: (54-11) 4580/7255/7
Fax: (54-11) 4752-9639
Email: dsanchez@lib.unsam.edu.ar
Sequences were basecalled with phred and vector was masked with
crossmatch (see http://www.phrap.org). Sequences were then trimmed
from both ends to remove low quality bases and masked vector.
Plate: 10 row: 1 column: 2
Seq primer: T7.
FEATURES
Location/Qualifiers
source
1..327
/organism="Trypanosoma carassii"
/mol_type="mRNA"
/db_xref="taxon:38249"
/clone="1012"
/dev_stages="blood trypomastigote"
/lab_host="Goldfish (Carassius auratus)"
/clone.lib="tca"
/note=Vector: pSport1; Blood trypomastigotes were
obtained from goldfish and cultured as described (Overath
et al. Parasitol Res (1998) 84:1343) before obtaining total
RNA using TRIzol. cDNA library construction was made from
polyA+ mRNA using a poly-dT oligonucleotide as primer. The
cDNAs were cloned in a oriented manner using a commercial
kit (SuperScript Plasmid System for cDNA Synthesis and
Plasmid Cloning, Life Technologies)."

ORIGIN
Query Match      68.2%; Score 15; DB 13; Length 327;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TCGTTATCCGGGCAA 19
|||||
Db 229 TCGTTATCCGGGCAA 243

/clone.lib="zebrafish adult brain"
/note=Vector: pZiPFOX; Site 1: NotI; Site 2: SalI;
Original library was constructed in lambdaZiPFOX. Mass
excision of the cDNA library was performed to yield
pZiPFOX plasmids. Insert check was done in original
library."

ORIGIN
Query Match      68.2%; Score 15; DB 12; Length 283;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TCGTTATCCGGGCAA 19
|||||
Db 229 TCGTTATCCGGGCAA 243

RESULT 10
CE669510/c
LOCUS tigr-gss-dog-17000329315342 Dog Library Canis familiaris genomic,
genomic survey sequence.
DEFINITION
ACCESSION CE669510
VERSION CE669510.1 GI:36988494
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 420)
AUTHORS Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
Venter, O.C.
TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
MEDLINE 22875432
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
Location/Qualifiers
source
1..420
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone.lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"

ORIGIN
Query Match      68.2%; Score 15; DB 29; Length 420;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCTTATCCGG 15
|||||
Db 93 CTTGCTTATCCGG 79

RESULT 11
AV661308/c
LOCUS AV661308 GLC Homo sapiens cDNA clone GLOCRA09 3', mRNA sequence.
DEFINITION
ACCESSION AV661308
VERSION AV661308.1 GI:9882322
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 432)
AUTHORS Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.,
Xiao, H., Qu, J., Liu, F., Huang, O., Cheng, Z., Li, N., Du, J., Hu, W.,
Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X.,
Hu, G., Gu, J., Chen, Z. and Han, Z.
TITLE Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
MEDLINE 21625106

```

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|||||
83 TCGTTATCCGGGCAA 69

CE669510
tigr-gss-dog-17000329315342 Dog Library Canis familiaris genomic,
genomic survey sequence.
DEFINITION
ACCESSION CE669510
VERSION CE669510.1 GI:36988494
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 420)
AUTHORS Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
Venter, O.C.
TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
MEDLINE 22875432
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
Location/Qualifiers
source
1..420
/organism="Canis familiaris"
/mol_type="genomic DNA"
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peripheral blood"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCTTATCCGG 15
|||||
Db 93 CTTGCTTATCCGG 79

RESULT 11
AV661308/c
LOCUS AV661308 GLC Homo sapiens cDNA clone GLOCRA09 3', mRNA sequence.
DEFINITION
ACCESSION AV661308
VERSION AV661308.1 GI:9882322
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 432)
AUTHORS Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.,
Xiao, H., Qu, J., Liu, F., Huang, O., Cheng, Z., Li, N., Du, J., Hu, W.,
Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X.,
Hu, G., Gu, J., Chen, Z. and Han, Z.
TITLE Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
MEDLINE 21625106

```

11752456
 PUBMED
 COMMENT
 Contact: Zequang Han
 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel: 86-21-50801919 (ex.45)
 Fax: 86-21-50801922
 Email: hanzg@chgc.sh.cn
 This clone is available at CHGC in Shanghai.

FEATURES
 source
 1. .432
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="GLCGRA09"
 /tissue_type="corresponding non cancerous liver tissue"
 /dev_stage="Adult"
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 /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"

ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CTTATCGGGCAAGA 21
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 Db 96 CTTATCGGGCAAGA 82
 |||||

RESULT 12
 CB818132/c
 LOCUS
 DEFINITION
 Plumbago zeylanica sperm cell (Svn) cDNA library
 Plumbago zeylanica cDNA clone a8f10p2 5', mRNA sequence.
 ACCESSION
 CB818132
 VERSION
 CB818132.1 GI:29950337
 KEYWORDS
 EST.
 SOURCE
 Plumbago zeylanica
 ORGANISM
 Plumbago zeylanica
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Plumbaginaceae; Plumbago.
 1 (bases 1 to 432)
 /organism="Plumbago zeylanica"
 /mol_type="mRNA"
 /db_xref="taxon:76149"
 /clone="a8f10p2"
 /cell_type="sperm cell"
 /dev_stage="post-anthesis pollen"
 /lab_host="E.coli strain XLI-Blue"
 /clone_lib="Plumbago zeylanica sperm cell (Svn) cDNA library"
 /note="Vector: Clontech Triplex2; Sua and Svn sperm cells were isolated and collected in separate pools using a microinjector. cDNA libraries were constructed by oligo dT

11752456
 PUBMED
 COMMENT
 Contact: Zequang Han
 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel: 86-21-50801919 (ex.45)
 Fax: 86-21-50801922
 Email: hanzg@chgc.sh.cn
 This clone is available at CHGC in Shanghai.

FEATURES
 source
 1. .432
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="GLCGRA09"
 /tissue_type="corresponding non cancerous liver tissue"
 /dev_stage="Adult"
 /lab_host="SOLR"
 /clone_lib="GLC"
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ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CTTATCGGGCAAGA 21
 |||||
 Db 96 CTTATCGGGCAAGA 82
 |||||

RESULT 12
 CB818132/c
 LOCUS
 DEFINITION
 Plumbago zeylanica sperm cell (Svn) cDNA library
 Plumbago zeylanica cDNA clone a8f10p2 5', mRNA sequence.
 ACCESSION
 CB818132
 VERSION
 CB818132.1 GI:29950337
 KEYWORDS
 EST.
 SOURCE
 Plumbago zeylanica
 ORGANISM
 Plumbago zeylanica
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Plumbaginaceae; Plumbago.
 1 (bases 1 to 432)
 /organism="Plumbago zeylanica"
 /mol_type="mRNA"
 /db_xref="taxon:76149"
 /clone="a8f10p2"
 /cell_type="sperm cell"
 /dev_stage="post-anthesis pollen"
 /lab_host="E.coli strain XLI-Blue"
 /clone_lib="Plumbago zeylanica sperm cell (Svn) cDNA library"
 /note="Vector: Clontech Triplex2; Sua and Svn sperm cells were isolated and collected in separate pools using a microinjector. cDNA libraries were constructed by oligo dT

priming using the Clontech SMART cDNA Library Construction kit. The cDNAs were directionally cloned into vector Triplex2."

ORIGIN
 Query Match 68.2%; Score 15; DB 14; Length 432;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTGTGCTTATCCGGG 16
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 Db 200 TTGTGCTTATCCGGG 186
 |||||

RESULT 13
 AG222515
 LOCUS
 DEFINITION
 Lotus corniculatus var. japonicus DNA, clone:LjB07e12_1, genomic survey sequence.
 ACCESSION
 AG222515
 VERSION
 AG222515.1 GI:26529924
 KEYWORDS
 GSS.
 SOURCE
 Lotus corniculatus var. japonicus (Lotus japonicus)
 ORGANISM
 Lotus corniculatus var. japonicus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
 Lotus.
 1
 Sato, S., Nakamura, Y. and Tabata, S.
 Lotus japonicus BAC End sequences
 Published Only in Database (2002)
 REFERENCE
 2 (bases 1 to 444)
 AUTHORS
 Sato, S.
 TITLE
 Direct Submission
 JOURNAL
 Submitted (20-NOV-2002) Shusei Sato, Kazusa DNA Research Institute,
 The First Laboratory for Plant Gene Research; 2-6-7
 Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan
 (E-mail:ssato@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/,
 Tel:81-438-52-3935(ex.2336), Fax:81-438-52-3934)
 Location/Qualifiers
 1. .444
 /organism="Lotus corniculatus var. japonicus"
 /mol_type="genomic DNA"
 /strain="Miyakojima MG-20"
 /variety="japonicus"
 /db_xref="taxon:34305"
 /clone="LjB07e12 f"
 /clone_lib="genomic BAC library"
 /note="VECTOR:pBelOBAC11-synonym: Lotus japonicus"

ORIGIN
 Query Match 68.2%; Score 15; DB 29; Length 444;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTGTGCTTATCCGGG 16
 |||||
 Db 409 TTGTGCTTATCCGGG 423
 |||||

RESULT 14
 CA723251
 LOCUS
 DEFINITION
 wdr1f.pk002.g11 wdr1f Triticum aestivum cDNA clone wdr1f.pk002.g11 5' end, mRNA sequence.
 ACCESSION
 CA723251
 VERSION
 CA723251.1 GI:25445044
 KEYWORDS
 EST.
 SOURCE
 Triticum aestivum (bread wheat)
 ORGANISM
 Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Poideae; Triticeae; Triticum.
1 (bases 1 to 466)
Tingey, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z.,
Miao, G., Caraher, N. and Hanafey, M.K.
DuPont Wheat cDNA Sequence
Unpublished (2002)
Contact: Scott V. Tingey
Crop Genetics
E. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2602
Fax: 302-631-2607
Email: Scott.V.Tingey@USA.dupont.com
Seq primer: M13.
Location/Qualifiers
1..466
/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone="wdr1f.pk002.g11"
/tissue_type="root"
/lab_hosts="DH10B"
/clone_lib="wdr1f"
/note="Vector: pluescript SK+; Site 1: EcoRI; Site 2:
xhoI; Wheat (Triticum aestivum) developing root (full
length)"

ORIGIN
Query Match 68.2%; Score 15; DB 14; Length 466;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 TTATCCGGGCAAGAA 22
|||||
DB 329 TTATCCGGGCAAGAA 343

RESULT 15
CF040747
LOCUS 476 bp mRNA linear EST 17-JUL-2003
DEFINITION QCI17h09.YG QCI Zea mays cDNA clone QCI17h09, mRNA sequence.
ACCESSION CF040747
VERSION CF040747.1 GI:32935935
KEYWORDS EST.
SOURCE
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 476)
Zeaplante.
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (<http://www.genoplante.com>
and <http://genoplante-info.inbioigen.fr>).
Location/Qualifiers
1..476
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="F2"
/db_xref="taxon:4577"
/clone="QCI17h09"
/tissue_type="embryo"
/clone_lib="QCI"

ORIGIN
Query Match 68.2%; Score 15; DB 14; Length 476;

Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TTGTGCTTATCCGGG 16
|||||
DB 23 TTGTGCTTATCCGGG 37

Search completed: August 2, 2004, 20:28:05
Job time : 913.207 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 17:27:15 ; Search time 470.509 seconds
(without alignments)
1934.510 Million cell updates/sec

Title: US-10-068-067-19

Perfect score: 21

Sequence: 1 gcaagaacttctgaaataca 21

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

1: gb_ba.*

2: gb_hg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_nu.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rod.*

36: em_htg_mam.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	21	100.0	21	6	AX513220	AX513220 Sequence
2	21	100.0	21	6	AX513225	AX513225 Sequence
3	21	100.0	51	6	AX513217	AX513217 Sequence
4	21	100.0	51	6	AX513222	AX513222 Sequence
5	21	100.0	212	9	AF262303	AF262303 Homo sapi
6	21	100.0	260	9	AF224495	AF224495 Homo sapi
7	21	100.0	348	9	AF262299	AF262299 Homo sapi
8	21	100.0	406	9	AF262301	AF262301 Homo sapi
9	21	100.0	410	9	AF262302	AF262302 Homo sapi
10	21	100.0	436	9	AF262304	AF262304 Homo sapi
11	21	100.0	957	9	AF224496S1	AF224496 Homo sapi
12	21	100.0	1193	6	AR300122	AR300122 Sequence
13	21	100.0	1193	6	BD082061	BD082061 G-protein
14	21	100.0	1453	9	AF247360	AF247360 Homo sapi
15	21	100.0	2895	6	AX513212	AX513212 Sequence
16	21	100.0	2895	9	AF237380S1	AF237380 Homo sapi
17	21	100.0	177334	9	AC138069	AC138069 Homo sapi
18	21	100.0	197279	9	AC104439	AC104439 Homo sapi
19	21	100.0	220965	2	HSR312688	HSR312688 Homo sapi
20	18	85.7	1454	9	AF247359	AF247359 Homo sapi
21	17	81.0	6991	3	PFARHPR	PFARHPR Plasmodium
22	17	81.0	8241	3	AF323443	AF323443 Plasmodium
23	17	81.0	8256	3	AF323442	AF323442 Plasmodium
24	17	81.0	95556	9	HSJ73H14	AL080272 Human DNA
25	17	81.0	95613	2	AC020389	AC020389 Drosophila
26	17	81.0	121524	8	AF041468	AF041468 Guillard
27	17	81.0	128574	8	CSJN00199	AL663002 Oryza sat
28	17	81.0	155840	2	AC006495	AC006495 Drosophila
29	17	81.0	174518	2	AC141658	AC141658 Homo sapi
30	17	81.0	199044	3	AC009394	AC009394 Drosophila
31	17	81.0	224890	3	AE003721	AE003721 Drosophila
32	16	76.2	1301	8	AK103163	AK103163 Oryza sat
33	16	76.2	2145	8	AF180024	AF180024 Huperzia
34	16	76.2	3187	8	CHCRPS13	X05847 C.reinhardt
35	16	76.2	10305	1	AE002502	AE002502 Neisseria
36	16	76.2	10707	1	AE002316	AE002316 Chlamydia
37	16	76.2	10733	2	AC141923	AE009750 Pyrobacul
38	16	76.2	116673	2	AC141923	AC141923 Medicago
39	16	76.2	141111	8	AP002481	AP002481 Oryza sat
40	16	76.2	155085	8	AP005693	AP005693 Oryza sat
41	16	76.2	155327	9	AC138761	AC138761 Homo sapi
42	16	76.2	198756	9	AC087575	AC087575 Homo sapi
43	16	76.2	199035	2	AC022263	AC022263 Homo sapi
44	16	76.2	307343	1	AE016998	AE016998 Bacillus
45	16	76.2	349980	6	AX044033	AX044033 Sequence

ALIGNMENTS

RESULT 1	AX513220	AX513220	21 bp	DNA	linear	PAT 03-OCT-2002
LOCUS	Sequence 19 from Patent WO02062848.					
DEFINITION	AX513220					
ACCESSION	AX513220					
VERSION	AX513220.1	GI:23504283				
KEYWORDS						
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE 1						
AUTHORS	Rothenberg, M.E. and Zimmerman, N.					
TITLE	Regulation of cc chemokine receptor 3 (ccr3) expression					
JOURNAL	Patent: WO 02062848-A 19 15-AUG-2002;					

CHILDREN'S HOSPITAL MEDICAL CENTER (US)

FEATURES
source

1. .21
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 21; DB 6; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.047; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGAACTTATCGAATAACA 21

Db 1 GCAAGAACTTATCGAATAACA 21

RESULT 2

AX513225

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

ORIGIN

Query Match

Best Local Similarity

Mismatches

Qy

Db

RESULT 3

AX513217

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

ORIGIN

Query Match

Best Local Similarity

Mismatches

Qy

Db

RESULT 4

AX513222

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

ORIGIN

Best Local Similarity 100.0%; Pred. No. 0.046;

Mismatches 21; Conservative 0; Indels 0; Gaps 0;

Qy 1 GCAAGAACTTATCGAATAACA 21

Db 31 GCAAGAACTTATCGAATAACA 51

RESULT 4

AX513222

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

ORIGIN

Query Match

Best Local Similarity

Mismatches

Qy

Db

RESULT 5

AF262303

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

ORIGIN

Query Match

Best Local Similarity

Mismatches

Qy

Db

RESULT 6

AF262303

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

ORIGIN

Query Match

Best Local Similarity

Mismatches

Qy

Db

RESULT 7

AF262303

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

ORIGIN

Query Match

Best Local Similarity

Mismatches

Qy

Db

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/map="3p21"
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1..>212
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/length=150..>212
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receptor expressed on eosinophils, CD4 Th2 lymphocytes,
CD8 lymphocytes, microglia, dendritic cells, and
monocytes"
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/product="CC chemokine receptor 3"
/protein_id="AAU85628.1"
/db_xref="GI:19171649"
/translation="MTTSLDTVETFGTTSYDDVG"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGAACTTATCGAATACA 21
|||||
Db 27 GCAAGAACTTATCGAATACA 47

RESULT 6
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LOCUS Homo sapiens CC chemokine receptor 3 (CCR3) mRNA, partial cds.
DEFINITION Homo sapiens CC chemokine receptor 3 (CCR3) mRNA, partial cds.
ACCESSION AF224495
VERSION AF224495.1 GI:13924481
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 260)
AUTHORS Scotet,E.J.
TITLE CCR3 expression is associated with chromatin remodeling in Th2
cells
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 260)
AUTHORS Scotet,E.J.
TITLE Direct Submission
JOURNAL Submitted (13-JAN-2000) Basel Institute for Immunology, 487
Grenzacherstrasse, Basel CH-4005, Switzerland
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ORIGIN
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Qy 1 GCAAGAACTTATCGAATACA 21
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Db 28 GCAAGAACTTATCGAATACA 48

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RESULT 7
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LOCUS Homo sapiens clone 1 CC chemokine receptor 3 (CCR3) mRNA, partial
DEFINITION cds.
ACCESSION AF262299
VERSION AF262299.1 GI:19171640
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 348)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.B., Imam,Z., Ehrenberg,P.K. and
Michael,N.L.
TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence
for a Rare TATA-less Promoter Structure Conserved between
Drosophila and Humans
Genomics 80 (1), 86-95 (2002)
JOURNAL MEDLINE
PUBMED 22074933
REFERENCE 2 (bases 1 to 348)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.B., Ehrenberg,P.K. and Michael,N.L.
TITLE Direct Submission
JOURNAL Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis,
Walter Reed Army Institute of Research, 1600 E. Gude Drive,
Rockville, MD 20850, USA
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1..>348
/gene="CCR3"
120..>348
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CD8 lymphocytes, microglia, dendritic cells, and
monocytes"
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/product="CC chemokine receptor 3"
/protein_id="AAU85628.1"
/db_xref="GI:19171641"
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Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGAACTTATCGAATACA 21
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Db 57 GCAAGAACTTATCGAATACA 77

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AF262301 406 bp mRNA linear PRI 26-JUN-2002
LOCUS Homo sapiens clone 4 CC chemokine receptor 3 (CCR3) mRNA, partial
DEFINITION cds.
ACCESSION AF262301
VERSION AF262301.1 GI:19171644
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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REFERENCE 1 (bases 1 to 406)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and Michael,N.L.
TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence for a Rare TATA-less Promoter Structure Conserved between Drosophila and Humans
JOURNAL Genomics 80 (1), 86-95 (2002)
MEDLINE 22074933
PUBMED 12079287

REFERENCE 2 (bases 1 to 406)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
TITLE Direct Submission
JOURNAL Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis, Walter Reed Army Institute of Research, 1600 E. Gude Drive, Rockville, MD 20850, USA

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/codon_start=1
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Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 28 GCAAGAACTTATCGAATAACA 48
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RESULT 9
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LOCUS AF262302 410 bp mRNA linear PRI 26-JUN-2002
DEFINITION Homo sapiens clone 5 CC chemokine receptor 3 (CCR3) mRNA, partial cds.
ACCESSION AF262302
VERSION AF262302.1 GI:19171646
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 410)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and Michael,N.L.
TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence for a Rare TATA-less Promoter Structure Conserved between Drosophila and Humans
JOURNAL Genomics 80 (1), 86-95 (2002)
MEDLINE 22074933
PUBMED 12079287

REFERENCE 2 (bases 1 to 410)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
TITLE Direct Submission

JOURNAL Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis, Walter Reed Army Institute of Research, 1600 E. Gude Drive, Rockville, MD 20850, USA

FEATURES
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Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGAACTTATCGAATAACA 21
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DB 28 GCAAGAACTTATCGAATAACA 48
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RESULT 10
AF262304
LOCUS AF262304 436 bp mRNA linear PRI 26-JUN-2002
DEFINITION Homo sapiens clone 7 CC chemokine receptor 3-like mRNA, partial sequence, alternatively spliced.
ACCESSION AF262304
VERSION AF262304.1 GI:19171650
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 436)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and Michael,N.L.
TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence for a Rare TATA-less Promoter Structure Conserved between Drosophila and Humans
JOURNAL Genomics 80 (1), 86-95 (2002)
MEDLINE 22074933
PUBMED 12079287

REFERENCE 2 (bases 1 to 436)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
TITLE Direct Submission
JOURNAL Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis, Walter Reed Army Institute of Research, 1600 E. Gude Drive, Rockville, MD 20850, USA

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ACCESSION AF224496
VERSION AF224496.1 GI:13924485
KEYWORDS
SEGMENT i of 2
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 957)
AUTHORS Scotet,E.J.
TITLE CCR3 expression is associated with chromatin remodeling in Th2
  cells
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 957)
AUTHORS Scotet,E.J.
TITLE Direct Submission
JOURNAL Submitted (13-JAN-2000) Basel Institute for Immunology, 487
  Grenzachstrasse, Basel CH-4005, Switzerland
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RESULT 12
AR300122 1193 bp mRNA linear PAT 12-JUN-2003
DEFINITION Sequence 3 from patent US 6537764.
ACCESSION AR300122
VERSION AR300122.1 GI:11687431
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1193)
AUTHORS Gerard,C.J., Gerard,N.P., Mackay,C.R., Ponath,P.D., Post,T.W. and
  Qin,S
TITLE Method of identifying inhibitors of C-C chemokine receptor 3
JOURNAL Patent: US 6537764-A 3 25-MAR-2003;
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RESULT 13
LOCUS BD082061 1193 bp DNA linear PAT 27-AUG-2002
DEFINITION G-protein coupled receptor antagonists.
ACCESSION BD082061
VERSION BD082061.1 GI:22627671
KEYWORDS JP 2001524068-A/2.
SOURCE Zea mays
ORGANISM Zea mays
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
  clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1193)
AUTHORS Mackay,C.R. and Ponath,P.D.
TITLE G-protein coupled receptor antagonists
JOURNAL Patent: JP 2001524068-A 2 27-NOV-2001;
  LEUKOSITE INC
COMMENT PN JP 2001524068-A/2
  PD 27-NOV-2001
  PF 24-SEP-1997 JP 1998516642
  PR 30-SEP-1996 US 08/720565
  PI CHARLES R MACKAY, PAUL D PONATH
  PC C07K16/18;C07K16/28;A61K39/395
  CC Strandedness: Double;
  CC Topology: Linear;
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Db 15 GCAAGAACTTATCGAAATACA 35

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AF247360 1453 bp DNA linear PRI 26-JUN-2002
LOCUS Homo sapiens CC chemokine receptor 3 (CCR3) gene, promoter region
DEFINITION and partial sequence.
ACCESSION AF247360
VERSION AF247360.1 GI:19110541
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1453)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and
  Michael,N.L.
TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence
  for a Rare TATA-less Promoter Structure Conserved between
  Drosophila and Humans

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Job time : 472.509 secs

JOURNAL Genomics 80 (1), 86-95 (2002)
MEDLINE 22074933
PUBMED 12079287
REFERENCE 2 (bases 1 to 1453)
AUTHORS Vijh.S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
TITLE Direct Submission
JOURNAL Submitted (21-MAR-2000) Dept. of Mol. Diag. and Pathogenesis, U.S.
Military HIV Research Program, 1600 E. Gude Drive, Rockville, MD
20850, USA

FEATURES
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Best Local Similarity 100.0%; Pred. No. 0.04; Mismatches 0; Indels 0; Gaps 0;
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RESULT 15
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LOCUS
DEFINITION Sequence 11 from Patent WO02062848.
ACCESSION AX513212
VERSION AX513212.1 GI:23504275
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Rothenberg M.E. and Zimmerman,N.
TITLE Regulation of cc chemokine receptor 3 (ccr3) expression
JOURNAL Patent: WO 02062848-A 11 15-AUG-2002;
CHILDREN'S HOSPITAL MEDICAL CENTER (US)
FEATURES
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Best Local Similarity 100.0%; Pred. No. 0.039; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0

QY 1 GCAAGAACTTATCGAATACA 21
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DB 1591 GCAAGAACTTATCGAATACA 1611

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 16:56:38 ; Search time 101.379 Seconds

(without alignments)
879.984 Million cell updates/sec

Title: US-10-068-067-19

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Searched: 337863 seqs, 2124099041 residues

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Minimum DB seq length: 0

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9: Geneseqn2003cs.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	21	100.0	21	6	ABQ78517 Nucleotid
3	21	100.0	51	6	ABQ78514 Nucleotid
4	21	100.0	51	6	ABQ78519 Nucleotid
5	21	100.0	1193	2	AAT31335 CC-chemok
6	21	100.0	1193	2	AAV07403 Human C-C
7	21	100.0	2895	6	ABQ78513 Nucleotid
8	17	81.0	2140	4	ABL12512 Drosophil
9	17	81.0	4400	4	ABL12414 Drosophil
10	16	76.2	5532	3	AA81538 N. mening
11	16	76.2	110000	3	AA81489 1
12	16	76.2	349980	3	AA81489 1
13	15	71.4	537	3	AA81489 1
14	15	71.4	864	7	ACF70596 Cat flea
15	15	71.4	1056	4	ACF70596 Phototrab
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C	25	15	71.4	265118	5	AAH41227	Aah41227 Pyrococcu
C	26	14	66.7	237	7	ACF70657	Acf70657 Phototrab
C	27	14	66.7	538	2	AA330895	Aax30895 Streptoco
C	28	14	66.7	564	7	ACA29622	Aca29622 Prokaryot
C	29	14	66.7	647	6	ABQ65988	Abq65988 Arabidops
C	30	14	66.7	669	6	ABN69167	Abn69167 Streptoco
C	31	14	66.7	669	6	ABN69168	Abn69168 Streptoco
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C	33	14	66.7	893	6	ABQ76400	Abq76400 S. cerevi
C	34	14	66.7	898	4	AA557071	Aas57071 C. tracho
C	35	14	66.7	898	9	ADD42725	Ad42725 Chlamydia
C	36	14	66.7	1338	7	ACA24565	Aca24565 Prokaryot
C	37	14	66.7	1374	3	AA70165	Aa70165 Plasmodiu
C	38	14	66.7	1545	3	AAFI2974	Aafi2974 Aspergill
C	39	14	66.7	1548	7	ABX06868	Abx06868 S. pneumo
C	40	14	66.7	1566	7	ACA49927	Aca49927 Prokaryot
C	41	14	66.7	2177	2	AA210370	Aa210370 DNA encod
C	42	14	66.7	2354	4	AA557070	Aas57070 C. tracho
C	43	14	66.7	2354	9	ADD42724	Ad42724 Chlamydia
C	44	14	66.7	2424	4	AA06040	Aad06040 Yeast YAK
C	45	14	66.7	2771	7	AA053418	Aad53418 Aspergill

ALIGNMENTS

RESULT 1

ABQ78587

ID ABQ78587 standard; RNA; 21 BP.

XX AC ABQ78587;

XX DT 25-NOV-2002 (first entry)

XX DE Nucleotide sequence of a regulatory sequence for human CCR3.

XX KW Human; CC chemokine receptor 3; CCR3; allergic disorder; probe;

XX KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;

XX KW infectious disorder; HIV; respiratory syncytial virus infection; ss.

XX OS Homo sapiens.

XX PN WO200262848-A2.

XX PD 15-AUG-2002.

XX PF 06-FEB-2002; 2002WO-US003442.

XX PR 07-FEB-2001; 2001US-0267073P.

XX PR 05-FEB-2002; 2002US-00068067.

XX PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

XX PI Rothenberg ME, Zimmerman N;

XX WPI; 2002-657524/70.

XX DR WPI; 2002-657524/70.

XX XX New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated

XX PT exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable

XX PT of binding to regulatory elements, useful for preventing e.g. allergic

XX PT inflammatory reactions.

XX XX Claim 8; Page 56; 56pp; English.

XX PS Claim 8; Page 56; 56pp; English.

XX CC The present sequence represents a probe for the human CC chemokine

XX CC receptor 3 (CCR3) gene. The probe is a regulatory sequence for CCR3. CCR3

XX CC is expressed on cells involved in allergic and/or inflammatory disorders.

XX CC The gene comprises 4 exons, with the coding region present on exon 4. The

XX CC specification describes methods of regulating the expression of CCR3. The

XX CC regulatory site is derived from an untranslated exon 1, exon 2, exon 3 or

XX CC promoter of a human CCR3 gene. Regulating the expression of the chemokine

XX CC receptor CCR3 is useful for preventing or treating disorders involving

CC eosinophils, such as allergic inflammatory and hypersensitivity
 CC reactions, certain types of leukemia, and certain infectious disorders
 CC involving CCR3, e.g. HIV or respiratory syncytial virus infection.
 CC Expression and modulation of CCR3 is a useful tool in assessing
 CC eosinophil targeting and in regulating eosinophil-mediated reactions and
 CC diseases
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 SQ Sequence 21 BP; 10 A; 4 C; 3 G; 0 T; 4 U; 0 Other;

Query Match 100.0%; Score 21; DB 6; Length 21;
 Best Local Similarity 81.0%; Pred. No. 0.025;
 Matches 17; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 GCAAGAACTTATCGAATAACA 21

RESULT 2
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 ID ABQ78517 standard; DNA; 21 BP.
 XX
 AC ABQ78517;
 XX
 DT 25-NOV-2002 (first entry)
 XX
 DE Nucleotide sequence of a regulatory sequence for human CCR3.
 XX
 KW Human; CC chemokine receptor 3; CCR3; allergic disorder; probe;
 KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;
 KW infectious disorder; HIV; respiratory syncytial virus infection; ss.
 XX
 OS Homo sapiens.

XX WO200262848-A2.
 XX 15-AUG-2002.
 XX
 XX 06-FEB-2002; 2002WO-US003442.
 XX
 XX 07-FEB-2001; 2001US-0267073P.
 XX 05-FEB-2002; 2002US-00068067.
 XX
 XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 XX
 XX Rothenberg ME, Zimmerman N;
 XX WPI; 2002-657524/70.

XX New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated
 XX exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable
 XX of binding to regulatory elements, useful for preventing e.g. allergic
 XX inflammatory reactions.
 XX
 XX Claim 6; Page 54; 56pp; English.
 XX
 XX The present sequence represents a probe for the human CC chemokine
 XX receptor 3 (CCR3) gene. The probe is a regulatory sequence for CCR3. CCR3
 XX is expressed on cells involved in allergic and/or inflammatory disorders.
 XX The gene comprises 4 exons, with the coding region present on exon 4. The
 XX specification describes methods of regulating the expression of CCR3. The
 XX regulatory site is derived from an untranslated exon 1, exon 2, exon 3 or
 XX promoter of a human CCR3 gene. Regulating the expression of the chemokine
 XX receptor CCR3 is useful for preventing or treating disorders involving
 XX eosinophils, such as allergic inflammatory and hypersensitivity
 XX reactions, certain types of leukemia, and certain infectious disorders
 XX involving CCR3, e.g. HIV or respiratory syncytial virus infection.
 XX Expression and modulation of CCR3 is a useful tool in assessing
 XX eosinophil targeting and in regulating eosinophil-mediated reactions and
 XX diseases

XX Sequence 21 BP; 10 A; 4 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 6; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.025;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGAACTTATCGAATAACA 21
 DB 1 GCAAGAACTTATCGAATAACA 21

RESULT 3
 ABQ78514
 ID ABQ78514 standard; DNA; 51 BP.
 XX
 AC ABQ78514;
 XX
 DT 25-NOV-2002 (first entry)
 XX
 DE Nucleotide sequence of a regulatory sequence for human CCR3.
 XX
 KW Human; CC chemokine receptor 3; CCR3; allergic disorder; probe;
 KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;
 KW infectious disorder; HIV; respiratory syncytial virus infection; ss.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 XX misc_binding 24..27
 XX /tag= a
 XX /note= "transcription factor binding site for GATA"
 XX misc_binding 40..43
 XX /tag= b
 XX /note= "transcription factor binding site for GATA"
 XX
 XX WO200262848-A2.
 XX 15-AUG-2002.
 XX
 XX 06-FEB-2002; 2002WO-US003442.
 XX
 XX 07-FEB-2001; 2001US-0267073P.
 XX 05-FEB-2002; 2002US-00068067.
 XX
 XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 XX
 XX Rothenberg ME, Zimmerman N;
 XX WPI; 2002-657524/70.

XX New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated
 XX exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable
 XX of binding to regulatory elements, useful for preventing e.g. allergic
 XX inflammatory reactions.
 XX
 XX Claim 2; Page 25; 56pp; English.
 XX
 XX The present sequence represents a probe for the human CC chemokine
 XX receptor 3 (CCR3) gene. The probe comprises -10 to +60 of exon 1 of CCR3,
 XX and is a regulatory sequence for CCR3. CCR3 is expressed on cells
 XX involved in allergic and/or inflammatory disorders. The gene comprises 4
 XX exons, with the coding region present on exon 4. The specification
 XX describes methods of regulating the expression of CCR3. The regulatory
 XX site is derived from an untranslated exon 1, exon 2, exon 3 or promoter
 XX of a human CCR3 gene. Regulating the expression of the chemokine receptor
 XX CCR3 is useful for preventing or treating disorders involving
 XX eosinophils, such as allergic inflammatory and hypersensitivity
 XX reactions, certain types of leukemia, and certain infectious disorders
 XX involving CCR3, e.g. HIV or respiratory syncytial virus infection.
 XX Expression and modulation of CCR3 is a useful tool in assessing
 XX eosinophil targeting and in regulating eosinophil-mediated reactions and
 XX diseases

XX Sequence 51 BP; 13 A; 12 C; 11 G; 15 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 6; Length 51;
 Best Local Similarity 100.0%; Pred. No. 0.024;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGAACTTATCGAAATACA 21
 DB 31 GCAAGAACTTATCGAAATACA 51

RESULT 4

ABQ78519
 ID ABQ78519 standard; RNA; 51 BP.

AC ABQ78519;
 DT 25-NOV-2002 (first entry)
 DE Nucleotide sequence of a regulatory sequence for human CCR3.

XX Human; CC chemokine receptor 3; CCR3; allergic disorder; probe;
 KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;
 KW infectious disorder; HIV; respiratory syncytial virus infection; ss.
 XX Homo sapiens.

OS
 PN WO200262848-A2.

XX
 PD 15-AUG-2002.

XX 06-FEB-2002; 2002WO-US003442.

XX 07-FEB-2001; 2001US-0267073P.

PR 05-FEB-2002; 2002US-00068067.

XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

XX Rothenberg ME, Zimmerman N;

XX WPI; 2002-657524/70.

XX New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated
 PT exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable
 PT of binding to regulatory elements, useful for preventing e.g. allergic
 PT inflammatory reactions.

XX Claim 7; Page 56; 56pp; English.

XX The present sequence represents a probe for the human CC chemokine
 CC receptor 3 (CCR3) gene. The probe is a regulatory sequence for CCR3. CCR3
 CC is expressed on cells involved in allergic and/or inflammatory disorders.
 CC The gene comprises 4 exons, with the coding region present on exon 4. The
 CC specification describes methods of regulating the expression of CCR3. The
 CC regulatory site is derived from an untranslated exon 1, exon 2, exon 3 or
 CC promoter of a human CCR3 gene. Regulating the expression of the chemokine
 CC receptor CCR3 is useful for preventing or treating disorders involving
 CC eosinophils, such as allergic inflammatory and hypersensitivity
 CC reactions, certain types of leukemia, and certain infectious disorders
 CC involving CCR3, e.g. HIV or respiratory syncytial virus infection.
 CC Expression and modulation of CCR3 is a useful tool in assessing
 CC eosinophil targeting and in regulating eosinophil-mediated reactions and
 CC diseases

XX Sequence 51 BP; 13 A; 12 C; 11 G; 0 T; 15 U; 0 Other;

Query Match 100.0%; Score 21; DB 6; Length 51;
 Best Local Similarity 81.0%; Pred. No. 0.024;
 Matches 17; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGAACTTATCGAAATACA 21
 DB 31 GCAAGAACTTATCGAAATACA 51

RESULT 5

AAT31335
 ID AAT31335 standard; cDNA; 1193 BP.

XX AAT31335;

XX 15-NOV-1996 (first entry)

XX CC-chemokine receptor 3 cDNA clone.

XX CC-chemokine receptor 3; CKP-3; Eos-L2; inhibitor; antisense;
 KW antiinflammatory; eosinophil; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 92..1159

XX FT /*tag= a

XX FT variation 918..919

XX FT /*tag= b

XX FT /note= "CCR-3 cDNA clone has GC at positions 918-919,
 FT coding for serine (AGC) at position 276; a genomic clone
 FT has CG at these positions, coding for threonine (AGC)"

XX PN WO9622371-A2.

XX 25-JUL-1996.

XX 19-JAN-1996; 96WO-US000608.

XX 19-JAN-1995; 95US-00375199.

XX (LEUK-) LEUKOSITE INC.

PA (BGM) BRIGHAM & WOMENS HOSPITAL.

PA (CHIL-) CHILDRENS MEDICAL CENT.

XX Gerard CJ, Gerard NP, Mackay CR, Ponath PD, Post TW, Qin S;

XX WPI; 1996-354528/35.

XX P-PSDB; AAW03377.

XX Mammalian chemokine receptor-3 and related nucleic acids - useful to
 PT identify receptor inhibitors to treat inflammatory disease, e.g.
 PT autoimmune disorders, certain cancers, etc.

XX Claim 1; Page 111-113; 153pp; English.

XX A genomic DNA clone (AAT31335) codes for a novel receptor (AAW03377),
 CC designated Eos L2 or C-C chemokine receptor 3 (CCR-3), involved in
 CC leukocyte migration associated with inflammation. It was isolated from a
 CC human library constructed from eosinophils obtd. from a patient with
 CC hyper-eosinophilic syndrome using a probe (p4 cDNA) encoding the MIP-
 CC alpha/RANTES receptor. A CCR-3 genomic clone (AAT31334) was also
 CC isolated, and a consensus sequence is given in AAT31336. The cDNA and
 CC genomic clones can be used for the prodn. of recombinant CCR-3 in host
 CC cells, or to design antisense sequences useful for treating inflammatory
 CC disease

XX Sequence 1193 BP; 274 A; 310 C; 275 G; 334 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 2; Length 1193;

Best Local Similarity 100.0%; Pred. No. 0.021;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGAACTTATCGAAATACA 21

DB 15 GCAAGAACTTATCGAAATACA 35

RESULT 6

AAV07403

ID AAV07403 standard; cDNA; 1193 BP.

XX

AC AAV07403;
 XX
 DT 28-SEP-1998 (first entry)
 XX Human C-C chemokine receptor 3 cDNA.
 XX
 XX C-C chemokine receptor 3; CCR3; Eos L2; human;
 KW G protein-coupled receptor; leukocyte; antibody; antagonist;
 KW inflammation; allergy; asthma; graft rejection; infection;
 KW autoimmune disease; drug screening; therapy; ds.
 XX
 OS Homo sapiens.
 XX
 XX KEY Location/Qualifiers
 FT 92..1159
 FT CDS /*tag= a
 XX
 XX WO9814480-A1.
 XX
 XX 09-APR-1998.
 XX
 XX 24-SEP-1997; 97WO-US017103.
 XX
 XX 30-SEP-1996; 96US-00720565.
 XX
 XX (LEUK-) LEUKOSITE INC.
 XX
 XX Mackay CR, Ponath PD;
 XX
 XX WPI; 1998-286418/25.
 DR P-PSDB; AAW51745.
 DR
 XX Antibodies to chemokine receptor-3 protein - useful for diagnosis and
 PT treatment of inflammatory conditions, e.g. allergy, asthma, autoimmune
 PT disease, graft rejection or cancer.
 PT
 XX Example 8; Page 134-136; 185pp; English.
 PS
 XX This cDNA codes for novel human C-C chemokine receptor 3 (see AAW51745),
 CC also designated CCR-3, CCR3 or Eos L2, that binds and mediates chemotaxis
 CC in response to chemokines such as eotaxin, RANTES and MCP-3. The cDNA was
 CC isolated from a human eosinophil cDNA library constructed from
 CC eosinophils obtained from a patient with hypereosinophilic syndrome, and
 CC using CCR-1 cDNA as probe. A genomic DNA sequence (see AAV07402) is also
 CC provided as well as a consensus sequence (see AAV07404) for CCR-3. The
 CC invention relates to isolated and/or recombinant nucleic acids encoding
 CC CCR-3, isolated or recombinant CCR-3 polypeptides, recombinant nucleic
 CC acid constructs, host cells useful for production of recombinant CCR-3
 CC proteins, to antibodies reactive with the receptors, and to methods of
 CC using these products to identify ligands, antagonists and agonists of
 CC receptor function. Inhibitors of CCR-3 can be used to treat: inflammatory
 CC or allergic diseases and conditions, including respiratory allergic
 CC diseases such as asthma, allergic rhinitis, hypersensitivity lung
 CC disease, hypersensitivity pneumonitis, eosinophilic pneumonia (e.g.
 CC Loeffler's syndrome, chronic eosinophilic pneumonia, interstitial lung
 CC disease (ILD) e.g. idiopathic pulmonary fibrosis or ILD associated with
 CC rheumatoid arthritis, systemic lupus erythematosus, ankylosing
 CC spondylitis, systemic sclerosis, Sjogren's syndrome, polymyositis or
 CC dermatomyositis), systemic anaphylaxis or hypersensitivity responses,
 CC drug allergy, insect sting allergy, inflammatory bowel disease, such as
 CC Crohn's disease and ulcerative colitis, spondyloarthropathy, scleroderma,
 CC psoriasis, inflammatory dermatosis such as dermatitis, eczema, atopic
 CC dermatitis, allergic contact dermatitis, urticaria, vasculitis (e.g.
 CC necrotizing cutaneous and hypersensitivity vasculitis); eosinophilic
 CC myositis and eosinophilic fasciitis; autoimmune diseases such as
 CC rheumatoid arthritis, psoriatic arthritis, multiple sclerosis, systemic
 CC lupus erythematosus, myasthenia gravis, juvenile onset diabetes,
 CC glomerulonephritis, autoimmune thyroiditis and Behcet's disease; graft
 CC rejection, including allograft rejection or graft-versus-host disease;
 CC cancers with leukocyte infiltration of the skin or organs; and also
 CC reperfusion injury, atherosclerosis, certain haematologic malignancies,
 CC septic shock and endotoxic shock. Promoters of CCR-3 function can be used
 CC for treating: immunosuppression e.g. in AIDS patients or individuals

CC undergoing radiation therapy, chemotherapy, therapy for autoimmune
 CC disease or other drug therapy, and immunosuppression due congenital
 CC deficiency in receptor function or other causes; and infectious diseases
 CC such as parasitic diseases, including helminth infections, such as
 CC nematodes (round worms). The agents can also be used for detection and
 CC diagnosis
 XX
 SQ Sequence 1193 BP; 274 A; 310 C; 275 G; 334 T; 0 U; 0 Other;
 Query Match 100.0%; Score 21; DB 2; Length 1193;
 Best Local Similarity 100.0%; Pred. NO. 0.021;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCAAGAACTTATCGAAATACA 21
 Db 15 GCAAGAACTTATCGAAATACA 35
 RESULT 7
 ABQ78513
 ID ABQ78513 standard; DNA; 2895 BP.
 XX
 AC ABQ78513;
 XX
 DT 25-NOV-2002 (first entry)
 XX
 DE Nucleotide sequence of the human CCR3 gene promoter.
 KW Human; CC chemokine receptor 3; CCR3; allergic disorder;
 KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;
 KW infectious disorder; HIV; respiratory syncytial virus infection;
 KW promoter; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT misc_signal 1640..1645
 FT /*tag= a
 FT /note= "splice donor consensus site"
 XX
 PN WO200262848-A2.
 PD
 PD 15-AUG-2002.
 XX
 XX 06-FEB-2002; 2002WO-US003442.
 XX
 XX 07-FEB-2001; 2001US-0267073P.
 XX
 XX 05-FEB-2002; 2002US-00068067.
 XX
 XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 XX
 XX Rothenberg ME, Zimmerman N;
 XX
 XX WPI; 2002-657524/70.
 XX
 XX New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated
 XX exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable
 XX of binding to regulatory elements, useful for preventing e.g. allergic
 XX inflammatory reactions.
 XX
 XX Disclosure; Fig 4; 56pp; English.
 XX
 XX The present sequence represents the promoter of the human CC chemokine
 XX receptor 3 (CCR3) gene. CCR3 is expressed on cells involved in allergic
 XX and/or inflammatory disorders. The gene comprises 4 exons, with the
 XX coding region present on exon 4. The specification describes methods of
 XX regulating the expression of CCR3. The regulatory site is derived from an
 XX untranslated exon 1, exon 2, exon 3 or promoter of a human CCR3 gene.
 XX Regulating the expression of the chemokine receptor CCR3 is useful for
 XX preventing or treating disorders involving eosinophils, such as allergic
 XX inflammatory and hypersensitivity reactions, certain types of leukemia,
 XX and certain infectious disorders involving CCR3 e.g. HIV or respiratory
 XX syncytial virus infection. Expression and modulation of CCR3 is a useful

CC tool in assessing eosinophil targeting and in regulating eosinophil-mediated reactions and diseases

XX Sequence 2895 BP; 829 A; 590 C; 556 G; 920 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 6; Length 2895;

Best Local Similarity 100.0%; Pred. No. 0.02;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAACTTATCGAAATACA 21
|||||

Db 1591 GCAGAACTTATCGAAATACA 1611

RESULT 8

ABL12512/c

ID ABL12512 standard; cDNA; 3140 BP.

XX AC ABL12512;

XX DT 26-MAR-2002 (first entry)

XX DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 32018.

XX KW Drosophila; developmental biology; cell signalling; insecticide;

XX KW pharmaceutical; gene; ss.

XX OS Drosophila melanogaster.

XX PN WO200171042-A2.

XX PD 27-SEP-2001.

XX PF 23-MAR-2001; 2001WO-US009231.

XX PR 23-MAR-2000; 2000US-0191637P.

XX PR 11-JUL-2000; 2000US-00614150.

XX PA (PEKE) PE CORP NY.

XX PI Venter JC, Adams M, Li PWD, Myers EW;

XX DR WPI; 2001-656860/75.

XX DR P-PSDB; ABB68409.

XX PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.

XX PS Claim 1; SEQ ID NO 32018; 21pp + Sequence Listing; English.

XX CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 3140 BP; 789 A; 738 C; 769 G; 844 T; 0 U; 0 Other;

Query Match 81.0%; Score 17; DB 4; Length 3140;

Best Local Similarity 100.0%; Pred. No. 3.3;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AGAACTTATCGAAATA 19
|||||

Db 2243 AGAACTTATCGAAATA 2227

RESULT 9

ABL12414/c

ID ABL12414 standard; cDNA; 4400 BP.

XX AC ABL12414;

XX DT 26-MAR-2002 (first entry)

XX DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 31724.

XX KW Drosophila; developmental biology; cell signalling; insecticide;

XX KW pharmaceutical; gene; ss.

XX OS Drosophila melanogaster.

XX PN WO200171042-A2.

XX PD 27-SEP-2001.

XX PF 23-MAR-2001; 2001WO-US009231.

XX PR 23-MAR-2000; 2000US-0191637P.

XX PR 11-JUL-2000; 2000US-00614150.

XX PA (PEKE) PE CORP NY.

XX PI Venter JC, Adams M, Li PWD, Myers EW;

XX DR WPI; 2001-656860/75.

XX DR P-PSDB; ABB68311.

XX PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.

XX PS Claim 1; SEQ ID NO 31724; 21pp + Sequence Listing; English.

XX CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 4400 BP; 1037 A; 1066 C; 1109 G; 1188 T; 0 U; 0 Other;

Query Match 81.0%; Score 17; DB 4; Length 4400;

Best Local Similarity 100.0%; Pred. No. 3.3;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AGAACTTATCGAAATA 19
|||||

Db 765 AGAACTTATCGAAATA 749

RESULT 10

AAA81538/c

ID AAA81538 standard; DNA; 5532 BP.

XX AC AAA81538;

XX DT 04-DEC-2000 (first entry)

XX DE N. meningitidis partial DNA sequence grm_95 SEQ ID NO:85.

XX KW Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;

XX KW antigen; vaccine; diagnosis; infection; antibacterial; identification;

XX KW Meningococcus B; MenB; ds.

OS Neisseria meningitidis.
 XX WO200022430-A2.
 XX
 XX
 XX 20-APR-2000.
 XX
 XX 08-OCT-1999; 99WO-US023573.
 XX
 XX 09-OCT-1998; 98US-0103794P.
 XX 30-APR-1999; 99US-0132068P.
 XX
 XX (CHIR) CHIRON CORP.
 XX
 XX
 XX Frazer CM, Hickey E, Peterson J, Tettelin H, Venter JC;
 XX Masignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;
 XX Rappuoli R, Pizza M;
 XX WPI; 2000-318079/27.
 XX
 XX Isolated nucleotide sequences of Neisseria meningitidis which can be used
 XX in the diagnosis and treatment of N. meningitidis infection and other
 XX Neisserial infections, for example, N.gonorrhoea.
 XX
 XX Claim 7; Page 1480-1482; 1760pp; English.
 XX
 XX The present invention describes methods of obtaining immunogenic proteins
 XX from Neisseria genomic sequences. AAA81453 to AAA82414 represent
 XX specifically claimed Neisseria meningitidis genomic DNA sequences;
 XX AAA81260 to AAA81303 and AA825620 to AA825663 represent Neisseria DNA
 XX sequences and their corresponding proteins; AAA81254 to AAA81259 and
 XX AAA81304 to AAA81321 represent PCR primers used in the isolation of
 XX Neisseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent
 XX Neisseria meningitidis MenB polynucleotide ORF sequences, which are all
 XX used in the exemplification of the present invention. The nucleic acid
 XX sequences, protein sequences, and antibodies against them, can be used in
 XX the manufacture of a composition. The composition can be used as a
 XX medicament (or in the manufacture of a medicament) for treating,
 XX preventing or diagnosing infection due to Neisserial bacteria. For
 XX example, some of the identified proteins could be components of vaccines
 XX against Meningococcus B; against all serotypes; and/or against all
 XX pathogenic Neisseriae. Identification of sequences from the bacterium
 XX will also facilitate production of biological probes, particularly
 XX organism-specific probes. Attempts to make efficacious Meningococcus B
 XX vaccines have failed mainly due to antigen tolerance. Multivalent
 XX vaccines have also been tried but none have successfully overcome
 XX antigenic variability. The provision of further, complete sequences may
 XX provide an opportunity to identify secreted or surface exposed proteins
 XX that may be presumed targets for the immune system and which are not
 XX antigenically variable or at least more conserved than other more
 XX variable regions
 XX
 XX SQ Sequence 5532 BP; 1241 A; 1503 C; 1452 G; 1336 T; 0 U; 0 Other;
 XX
 XX Query Match 76.2%; Score 16; DB 3; Length 5532;
 XX Best Local Similarity 100.0%; Pred. No. 12;
 XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 GCAAGAACTTATCGAA 16
 XX |||||
 XX 2627 GCAAGAACTTATCGAA 2612
 XX
 XX RESULT 11
 XX AAA81489_1/c
 XX Continuation (2 of 9) of AAA81489 from base 100001 (N. meningitidis partial DNA sequence
 XX Sequence split into 9 fragments LOCUS AAA81489 Accession AAA81489
 XX Fragment Name Begin End
 XX WP AAA81489_0 1 110000
 XX WP AAA81489_1 100001 210000
 XX WP AAA81489_2 200001 310000
 XX WP AAA81489_3 300001 410000
 XX WP AAA81489_4 400001 510000
 XX WP AAA81489_5 500001 610000

WP AAA81489_6 600001 710000
 WP AAA81489_7 700001 810000
 WP AAA81489_8 800001 937096
 XX
 XX Query Match 76.2%; Score 16; DB 3; Length 110000;
 XX Best Local Similarity 100.0%; Pred. No. 10;
 XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 GCAAGAACTTATCGAA 16
 XX |||||
 XX 45992 GCAAGAACTTATCGAA 45977
 XX
 XX Db
 XX
 XX RESULT 12
 XX AAF21611/c
 XX ID AAF21611 standard; DNA; 349980 BP.
 XX
 XX AC AAF21611;
 XX
 XX DT 13-MAR-2001 (first entry)
 XX
 XX DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:112.
 XX
 XX KW Neisseria meningitidis; Neisseria gonorrhoeae; immunogenic; vaccine;
 XX diagnosis; antigen; detection; infection; gene therapy; antibacterial;
 XX ds.
 XX OS Neisseria meningitidis.
 XX XX WO2000066791-A1.
 XX 09-NOV-2000.
 XX 08-MAR-2000; 2000WO-US005928.
 XX 30-APR-1999; 99US-0132068P.
 XX 08-OCT-1999; 99WO-US023573.
 XX 28-FEB-2000; 2000GB-00004695.
 XX (CHIR) CHIRON CORP.
 XX (GENO-) INST GENOMIC RES.
 XX
 XX Pizza M, Hickey E, Peterson J, Tettelin H, Venter JC;
 XX Masignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;
 XX Rappuoli R, Frazer CM, Grandi G;
 XX WPI; 2000-647603/62.
 XX
 XX Neisseria meningitidis B full length genome sequence and open reading
 XX frames are used to detect, treat and prevent Neisserial infections.
 XX
 XX Claim 7; Appendix A; 692pp; English.
 XX
 XX The present invention describes the full length genome of Neisseria
 XX meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613
 XX represent fragments of the NMB genomic sequence, as the sequences which
 XX long to go in a record on its own it was split into 8 sequences which
 XX overlap each other at the beginning and end of each sequence by 49980 bp
 XX (i.e. the last 49980 bp of AAF21544 is repeated at the beginning of
 XX AAF21607, the last 49980 bp of AAF21607 are repeated at the beginning of
 XX AAF21608, and so on). AAF21545 to AAF21588 encode the Neisseria proteins
 XX given in AAB58550 to AAB58593, and AAF21589 to AAF21606 represent PCR
 XX primers which are used in the exemplification of the present invention.
 XX The NMB genome and fragments from it have antibacterial activity, and can
 XX be used in vaccines and gene therapy. Neisseria nucleic acids, proteins
 XX and/or antibodies which binds to the proteins can be used in compositions
 XX for treating or preventing infection due to Neisserial bacteria or as a
 XX diagnostic reagent for detecting the presence of Neisserial bacteria or
 XX of antibodies raised to Neisserial bacteria. Computers, computer memory,
 XX computer storage medium or computer databases can be used in a search to
 XX identify open reading frames (ORFs) or coding sequences within the NMB
 XX genome. The DNA sequences provide further opportunities to find antigenic
 XX or immunogenic proteins which are more effective in vaccines than the

CC outer membrane proteins currently used

XX Sequence 349980 BP; 87189 A; 93501 C; 84627 G; 84663 T; 0 U; 0 Other;

SQ Query Match 76.2%; Score 16; DB 3; Length 349980;

Best Local Similarity 100.0%; Pred. No. 9.5;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGAACTTATCGAA 16

|||||

Db 81221 GCAAGAACTTATCGAA 81206

RESULT 13

AAC94557

ID AAC94557 standard; cDNA; 537 BP.

XX AC AAC94557;

XX AC AAC94557;

XX AC AAC94557;

DT 19-FEB-2001 (first entry)

DE Cat flea hindgut and Malpighian tubule (HMT) cDNA, SEQ ID NO:1052.

XX Cat flea; hindgut and Malpighian tubule nucleic acid; HMT;

KW flea infestation; vaccine; antiparasitic; therapeutic target; diagnosis;

KW detection; ss.

XX Ctenocephalides felis.

OS WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

XX WO2000061621-A2.

CC in samples (e.g., by enzyme linked immunosorbent assay (ELISA)). The

XX present sequence represents a cat flea HMT cDNA of the invention

SQ Sequence 537 BP; 164 A; 86 C; 101 G; 185 T; 0 U; 1 Other;

Query Match 71.4%; Score 15; DB 3; Length 537;

Best Local Similarity 100.0%; Pred. No. 48;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AACTTATCGAATAC 20

|||||

Db 144 AACTTATCGAATAC 158

RESULT 14

ACF70596

ID ACF70596 standard; DNA; 864 BP.

XX AC ACF70596;

XX AC ACF70596;

XX AC ACF70596;

DT 20-NOV-2003 (first entry)

DE Photorhabdus luminescens nucleotide sequence #9063.

XX Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;

KW detection; food; gene expression; plant; animal; microorganism; toxin;

KW antibiotic; biopesticide; virulence factor; disease model; plague;

XX whooping cough; gene; ds.

XX Photorhabdus luminescens.

OS WO200294867-A2;

XX WO200294867-A2;

XX WO200294867-A2;

XX WO200294867-A2;

XX WO200294867-A2;

XX WO200294867-A2;

XX WO200294867-A2;

XX WO200294867-A2;

XX WO200294867-A2;

XX WO200294867-A2;

XX WO200294867-A2;

XX WO200294867-A2;

XX WO200294867-A2;

XX WO200294867-A2;

XX WO200294867-A2;

XX WO200294867-A2;

XX WO200294867-A2;

XX WO200294867-A2;

XX WO200294867-A2;

XX WO200294867-A2;

XX WO200294867-A2;

XX WO200294867-A2;

XX WO200294867-A2;

XX WO200294867-A2;

PS Claim 2; SEQ ID NO 9063; 1205pp; French.

CC The invention relates to the isolation of genes and their encoded
CC proteins from Photorhabdus luminescens. The isolated sequences are
CC sources of probes and primers for detecting the genome of P. luminescens
CC and related species; to study polymorphisms; for gene analysis and for
CC detection/amplification of the genes. Antibodies (Ab) raised against the
CC polypeptides encoded by the genes are used for detection/identification
CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that
CC carry a gene-containing vector are used to select compounds that
CC modulate, regulate, induce or inhibit expression of the genes in plants,
CC animals or microorganisms other than P. luminescens and are able to alter
CC response or sensitivity to toxins and antibiotics produced by P.
CC luminescens. Cells transformed to express the genes are useful for
CC recombinant production of the proteins, particularly toxins and
CC antibacterials useful as insecticides, bactericides and fungicides. The
CC genes, proteins, vectors containing the genes and Ab are also useful
CC therapeutically to treat microbial infection by bacteria or fungi that
CC are sensitive to P. luminescens-encoded toxins or antibiotics and as
CC biopesticides. Other uses of the genes and the proteins are as virulence
CC factors and for identifying targets of human diseases for which P.
CC luminescens is a model (particularly plague and whooping cough). This
CC sequence represents one of the isolated P. luminescens genes

XX
SQ Sequence 864 BP; 251 A; 153 C; 188 G; 272 T; 0 U; 0 Other;
Query Match 71.4%; Score 15; DB 7; Length 864;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGAAGTTATCGAAA 17
|||||
Db 446 AAGAAGTTATCGAAA 460

RESULT 15
ABL25529
ID ABL25529 standard; DNA; 1056 BP.
XX
AC ABL25529;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 28060.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
PS Claim 1; SEQ ID NO 28060; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences)
XX
SQ Sequence 1056 BP; 227 A; 256 C; 249 G; 324 T; 0 U; 0 Other;
Query Match 71.4%; Score 15; DB 4; Length 1056;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAAGAAGTTATCGAA 16
|||||
Db 330 CAAGAAGTTATCGAA 344

Search completed: August 2, 2004, 18:24:30
Job time : 104.379 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 18:10:40 ; Search time 21.181 Seconds
(without alignments)
550.208 Million cell updates/sec

Title: US-10-068-067-19

Perfect score: 21

Sequence: 1 gcaagaacttcagaaataca 21

Scoring table: OLIGO NUC

Gapop_60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA.*

- 1: /cgn2_6/ptodata/2/ina/5A COMB.seq.*
- 2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*
- 3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq.*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	21	100.0	1193	4	US-08-720-565-3
2	15	71.4	8920	2	US-08-446-855A-1
3	15	71.4	8920	3	US-09-150-741-1
4	14	66.7	435	4	US-09-489-039A-6593
5	14	66.7	2793	4	US-08-753-750B-1
6	14	66.7	4820	4	US-08-961-527-19
7	14	66.7	45175	4	US-09-453-702B-116
8	14	65.7	129908	4	US-09-585-858-1
9	13	61.9	207	4	US-09-107-532A-1213
10	13	61.9	400	4	US-08-956-171E-1342
11	13	61.9	1056	3	US-09-293-395-10
12	13	61.9	1056	3	US-09-668-648-10
13	13	61.9	1474	4	US-08-858-207A-144
14	13	61.9	1479	4	US-09-107-532A-3408
15	13	61.9	2153	4	US-09-221-017B-984
16	13	61.9	2538	4	US-09-543-681A-193
17	13	61.9	2951	1	US-08-413-118-105
18	13	61.9	2951	3	US-08-473-446-105
19	13	61.9	5739	4	US-09-634-238-1
20	13	61.9	8703	4	US-08-961-527-177
21	13	61.9	640681	4	US-09-790-988-1
22	12	57.1	31	2	US-08-467-265-9
23	12	57.1	31	3	US-08-467-265-9
24	12	57.1	31	3	US-09-407-891-9
25	12	57.1	38	2	US-08-467-265-6
26	12	57.1	38	3	US-08-467-265-6
27	12	57.1	38	3	US-09-407-891-6

28 12 57.1 145 4 US-08-956-171E-3207 Sequence 3207, Ap
C 29 12 57.1 160 1 US-08-327-525A-19 Sequence 19, Appl
C 30 12 57.1 160 1 US-08-327-525A-25 Sequence 25, Appl
C 31 12 57.1 160 1 US-08-327-525A-26 Sequence 26, Appl
C 32 12 57.1 160 1 US-08-327-525A-27 Sequence 27, Appl
C 33 12 57.1 160 2 US-08-531-137B-19 Sequence 19, Appl
C 34 12 57.1 160 2 US-08-531-137B-25 Sequence 25, Appl
C 35 12 57.1 160 2 US-08-531-137B-26 Sequence 26, Appl
C 36 12 57.1 160 2 US-08-531-137B-27 Sequence 27, Appl
C 37 12 57.1 160 3 US-09-158-765-19 Sequence 19, Appl
C 38 12 57.1 160 3 US-09-158-765-25 Sequence 25, Appl
C 39 12 57.1 160 3 US-09-158-765-26 Sequence 26, Appl
C 40 12 57.1 160 3 US-09-158-765-27 Sequence 27, Appl
C 41 12 57.1 160 4 US-09-796-071-19 Sequence 19, Appl
C 42 12 57.1 160 4 US-09-796-071-25 Sequence 25, Appl
C 43 12 57.1 160 4 US-09-796-071-26 Sequence 26, Appl
C 44 12 57.1 160 4 US-09-796-071-27 Sequence 27, Appl
C 45 12 57.1 246 4 US-09-489-039A-4912 Sequence 4912, Ap

ALIGNMENTS

RESULT 1
US-08-720-565-3
; Sequence 3, Application US/08720565
; Patent No. 6537764
; GENERAL INFORMATION:
; APPLICANT: Gerard, Craig J.
; APPLICANT: Gerard, No. 6537764ma P.
; APPLICANT: Mackay, Charles R.
; APPLICANT: Ponath, Paul D.
; APPLICANT: Post, Theodore W.
; APPLICANT: Qin, Shixin
; TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTOR GENE CCR3 AND
; TITLE OF INVENTION: ANTAGONISTS THEREOF
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173

COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,565
FILING DATE: 30-SEP-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00608
FILING DATE: 19-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375,199
FILING DATE: 19-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LK994-05A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1193 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA

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;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 92..1156
; US-08-720-565-3

Query Match      100.0%; Score 21; DB 4; Length 1193;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGAACTTATCGAATACA 21
    |||||
Db 15 GCAAGAACTTATCGAATACA 35
    |||||

RESULT 2
US-08-446-855A-1
; Sequence 1, Application US/08446855A
; Patent No. 5849573
; GENERAL INFORMATION:
; APPLICANT: Stewart, Thomas S
; APPLICANT: Flores, Maria V
; APPLICANT: O'Sullivan, William J
; TITLE OF INVENTION: Nucleotide sequence encoding carbamoyl
; TITLE OF INVENTION: phosphate synthetase II
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vandethye PC
; STREET: 1100 No. 5849573th Glebe Road, 8th Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,855A
; FILING DATE: 06-Jul-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mitchard, Leonard C
; REGISTRATION NUMBER: 29.009
; REFERENCE/DOCKET NUMBER: 47-80
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8920 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic
; US-08-446-855A-1

Query Match      71.4%; Score 15; DB 2; Length 8920;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AAGAACTTATCGAAA 17
    |||||
Db 3831 AAGAACTTATCGAAA 3845
    |||||

RESULT 3
US-09-150-741-1
; Sequence 1, Application US/09150741
; Patent No. 618396
; GENERAL INFORMATION:
; APPLICANT: Stewart et al.
; TITLE OF INVENTION: Nucleotide Sequence Encoding Carbamoyl Phosphate

; Patent No. 618396
; TITLE OF INVENTION: Synthetase II
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/150,741
; CURRENT FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: PL6380
; EARLIER FILING DATE: 1992-12-16
; EARLIER APPLICATION NUMBER: AU93/00617
; EARLIER FILING DATE: 1993-12-02
; EARLIER APPLICATION NUMBER: 08/446,855
; EARLIER FILING DATE: 1995-07-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 8920
; TYPE: DNA
; ORGANISM: Plasmodium falciparum
; US-09-150-741-1

Query Match      71.4%; Score 15; DB 3; Length 8920;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AAGAACTTATCGAAA 17
    |||||
Db 3831 AAGAACTTATCGAAA 3845
    |||||

RESULT 4
US-09-489-039A-6593
; Sequence 6593, Application US/09489039A
; Patent No. 8610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709,2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 6593
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
; US-09-489-039A-6593

Query Match      66.7%; Score 14; DB 4; Length 435;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GAAGTATTCGAAT 18
    |||||
Db 85 GAAGTATTCGAAT 98
    |||||

RESULT 5
US-08-753-750B-1
; Sequence 1, Application US/08753750B
; Patent No. 8610506
; GENERAL INFORMATION:
; APPLICANT: Lo, Reggie Y.C.
; APPLICANT: Schryvers, Anthony B.
; APPLICANT: Potter, Andrew A.
; TITLE OF INVENTION: TRANSFERRIN BINDING PROTEINS OF
; TITLE OF INVENTION: PASTEURILLA HAEMOLYTICA AND VACCINES CONTAINING THE SAME
; FILE REFERENCE: A34762 021645.0105
; CURRENT APPLICATION NUMBER: US/08/753,750B
; CURRENT FILING DATE: 1996-11-29
; PRIOR APPLICATION NUMBER: CA 2,164,274
; PRIOR FILING DATE: 1995-12-01
; PRIOR APPLICATION NUMBER: 60/008,569
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;; PRIOR FILING DATE: 1995-12-01
;; NUMBER OF SEQ ID NOS: 58
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 1
;; LENGTH: 2793
;; TYPE: DNA
;; ORGANISM: Pasteurella haemolytica
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 2544
;; OTHER INFORMATION: a, c, g or t
US-08-753-750B-1

Query Match 66.7%; Score 14; DB 4; Length 2793;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GAACCTATCGAAAT 18
|||||
DB 1895 GAACCTATCGAAAT 1908

RESULT 6
US-08-961-527-19
; Sequence 19, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch

;; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
;; NUMBER OF SEQUENCES: 391
;; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.

;; STREET: 9410 Key West Avenue
;; CITY: Rockville
;; STATE: Maryland
;; COUNTRY: USA
;; ZIP: 20850

;; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; APPLICATION NUMBER: US/08/961.527
; FILING DATE:
; CLASSIFICATION: 424

;; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504

;; TELEFAX: (301) 309-8512
;; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4820 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear

US-08-961-527-19
Query Match 66.7%; Score 14; DB 4; Length 4820;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACTTATCGAAATAC 20
|||||
DB 3955 ACTTATCGAAATAC 3968

RESULT 7

US-09-453-702B-116/c
; Sequence 116, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.

;; Burland, Nicole T.
;; Perna, Valerie
;; Plunkett, Guy
;; Welch, Rod

;; TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
;; NUMBER OF SEQUENCES: 265
;; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady

;; STREET: 1 South Pinckney Street
;; CITY: Madison
;; STATE: WI
;; COUNTRY: US
;; ZIP: 53701-2113

;; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage

;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Word Perfect 8.0
;; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,702B

;; FILING DATE: 03-Dec-1999
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/110,955

;; FILING DATE: 04-DEC-1998
;; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.

;; REGISTRATION NUMBER: 27386
;; REFERENCE/DOCKET NUMBER: 960296.95017
;; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000

;; TELEFAX: (608) 251-9166
;; INFORMATION FOR SEQ ID NO: 116:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45175

;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; SEQUENCE DESCRIPTION: SEQ ID NO: 116:
US-09-453-702B-116

Query Match 66.7%; Score 14; DB 4; Length 45175;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGAACTTATCG 14
|||||
DB 34538 GCAAGAACTTATCG 34525

RESULT 8

US-09-585-858-1
; Sequence 1, Application US/09585858
; Patent No. 6492161
; GENERAL INFORMATION:
; APPLICANT: Sigrundur Hjorleifsdottir

;; Gudmundur O. Hreggvidsson
;; APPLICANT: Olafur H. Fridjonsson
;; APPLICANT: Arthor Aevarsson
;; APPLICANT: Jakob K. Kristjansson

;; TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
;; FILE REFERENCE: 2739.1001-001
;; CURRENT APPLICATION NUMBER: US/09/585,858
;; CURRENT FILING DATE: 2000-12-18
;; PRIOR APPLICATION NUMBER: 60/137,120

; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 129908
; TYPE: DNA
; ORGANISM: Bacteriophage RM378
US-09-585-858-1

Query Match 66.7%; Score 14; DB 4; Length 129908;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GAACCTTATCGAAT 18
| | | | | | | | | | | | | | | | | | | | | |
DB 11282 GAACCTTATCGAAT 11295

RESULT 9

US-09-107-532A-1213
; Sequence 1213 Application US/09107532A
; Patent No. 6593275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION

; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354

; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997

; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277

; INFORMATION FOR SEQ ID NO: 1213:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 207 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; ORGANISM: Enterococcus faecium

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (B) LOCATION 1...207

; SEQUENCE DESCRIPTION: SEQ ID NO: 1213:

US-09-107-532A-1213

Query Match 61.9%; Score 13; DB 4; Length 207;
Best Local Similarity 100.0%; Pred. No. 74;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCAAGAACTTATC 13
| | | | | | | | | | | | | | | | | | | | | |
DB 139 GCAAGAACTTATC 151

RESULT 10

US-08-956-171E-1342
; Sequence 1342 Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch

; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; ADDRESSEE: Human Genome Sciences, Inc.

; CORRESPONDENCE ADDRESS:
; STREET: 9410 Key West Avenue
; CITY: Rockville

; STATE: Maryland

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

; COMPUTER: HP Vectra 486/33

; OPERATING SYSTEM: MSDOS version 6.2

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/956,171E

; FILING DATE: 20-Oct-1997

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/009,861

; FILING DATE: January 5, 1996

; APPLICATION NUMBER: 08/781,986

; FILING DATE: January 3, 1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Mark J. Hyman

; REGISTRATION NUMBER: 46,789

; REFERENCE/DOCKET NUMBER: PB248P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (240) 314-1224

; TELEFAX: (301) 309-8439

; INFORMATION FOR SEQ ID NO: 1342:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 400 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 1342:

US-08-956-171E-1342

Query Match 61.9%; Score 13; DB 4; Length 400;

Best Local Similarity 100.0%; Pred. No. 73;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GAACCTTATCGAAA 17
| | | | | | | | | | | | | | | | | | | | | |

DB 87 GAACCTTATCGAAA 99

RESULT 11

US-09-293-395-10

; Sequence 10, Application US/09293395

; Patent No. 6174860

; GENERAL INFORMATION:

; APPLICANT: Kramer, Vance

; APPLICANT: Morgan, Michael

APPLICANT: Anderson, Arne
TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS
FILE REFERENCE: PB/5-30472A/USN
CURRENT APPLICATION NUMBER: US/09/293,395
CURRENT FILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 10
LENGTH: 1056
TYPE: DNA
ORGANISM: Xenorhabdus poinarii
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1053)
OTHER INFORMATION: JHE-like orf2 of pCIB9354
US-09-293-395-10

Query Match 61.9%; Score 13; DB 3; Length 1056;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGAACTTATCGA 15
|||||
Db 536 AAGAACTTATCGA 548

RESULT 12
US-09-668-648-10
Sequence 10, Application US/09668648
Patent No. 6277823
GENERAL INFORMATION:
APPLICANT: Kramex, Vance
APPLICANT: Morgan, Michael
APPLICANT: Anderson, Arne
TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS
FILE REFERENCE: PB/5-30472A/USN
CURRENT APPLICATION NUMBER: US/09/668,648
CURRENT FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 09/293,395
PRIOR FILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 10
LENGTH: 1056
TYPE: DNA
ORGANISM: Xenorhabdus poinarii
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1053)
OTHER INFORMATION: JHE-like orf2 of pCIB9354
US-09-668-648-10

Query Match 61.9%; Score 13; DB 3; Length 1056;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGAACTTATCGA 15
|||||
Db 536 AAGAACTTATCGA 548

RESULT 13
US-08-858-207A-144/c
Sequence 144, Application US/08858207A
Patent No. 6348328
GENERAL INFORMATION:
APPLICANT: Black, Michael
APPLICANT: Hodgson, John
APPLICANT: Knowles, David
APPLICANT: Nicholas, Richard
APPLICANT: Stodola, Robert

TITLE OF INVENTION: No. 6348328el Compounds
NUMBER OF SEQUENCES: 552
CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,207A
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R.
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P50475
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 144:
SEQUENCE CHARACTERISTICS:
LENGTH: 1474 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-858-207A-144

Query Match 61.9%; Score 13; DB 4; Length 1474;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGAACTTATCGA 15
|||||
Db 1135 AAGAACTTATCGA 1123

RESULT 14
US-09-107-532A-3408
Sequence 3408, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3408:
SEQUENCE CHARACTERISTICS:
LENGTH: 1479 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...1479
SEQUENCE DESCRIPTION: SEQ ID NO: 3408:

US-09-107-532A-3408

Query Match 61.9%; Score 13; DB 4; Length 1479;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACTTATCGAAATA 19

Db 1112 ACTTATCGAAATA 1124

RESULT 15

US-09-221-017B-984
Sequence 984, Application US/09221017B
Patent No. 644799
GENERAL INFORMATION:
APPLICANT: Ross, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA: P1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA: P22911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Monroy, Gladys H

REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27340-20021.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 850-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 984:
SEQUENCE CHARACTERISTICS:
LENGTH: 2153 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:
ORGANISM: PORYPHYROMONAS GINGIVALIS
FEATURE:
NAME/KEY: misc feature
LOCATION: 1...2153
US-09-221-017B-984

Query Match 61.9%; Score 13; DB 4; Length 2153;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AGAATTATCGAA 16

Db 1085 AGAATTATCGAA 1097

Search completed: August 2, 2004, 20:30:06
Job time : 22.181 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 18:06:45 ; Search time 867.879 Seconds

(without alignments)
722.573 Million cell updates/sec

Title: US-10-068-067-19

Perfect score: 21

Sequence: 1 gcaagaacttgcgaataca 21

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:

1: em_estba:*
2: em_esthm:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hci:*
9: gb_estl:*
10: gb_est2:*
11: gb_hci:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_lman:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gssl:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	876	12	BI906283
2	17	81.0	647	12	BM160641
3	16	76.2	288	9	AV340346
4	16	76.2	404	10	BE344124

5	16	76.2	406	12	BI179888
c	7	76.2	477	28	BH743658
9	16	76.2	486	12	BQ045539
10	16	76.2	487	10	BE471486
11	16	76.2	493	13	BX563981
12	16	76.2	517	12	BM407701
13	16	76.2	649	12	B435938
c	14	76.2	677	12	B435917
15	16	76.2	685	28	BZ387666
16	16	76.2	694	10	BG031536
17	16	76.2	712	9	AU057789
18	16	76.2	721	9	AL932228
19	16	76.2	737	12	BG599509
20	16	76.2	756	12	BG666673
21	16	76.2	796	14	CB674182
22	16	76.2	815	14	CK265108
c	23	76.2	829	10	BE622748
24	16	76.2	843	28	CC435132
25	16	76.2	845	14	CK276849
26	16	76.2	923	14	CK264361
27	15	71.4	967	14	CK272439
28	15	71.4	169	9	AV162852
c	29	71.4	299	29	BX288585
30	15	71.4	306	29	AL950150
31	15	71.4	323	29	CC812736
32	15	71.4	335	9	AU110785
33	15	71.4	340	28	BH697529
34	15	71.4	387	28	AQ440255
35	15	71.4	412	9	AA281990
c	36	71.4	424	28	BH833079
37	15	71.4	432	28	BH633995
38	15	71.4	446	9	AA139325
39	15	71.4	483	29	AL950151
c	40	71.4	491	28	AQ866738
41	15	71.4	498	14	CB336952
c	42	71.4	501	28	AQ866647
43	15	71.4	513	28	AZ929038
44	15	71.4	515	28	BH443715
45	15	71.4	516	13	BQ988753
			517	14	CB358701

ALIGNMENTS

BI906283 876 bp mRNA linear EST 16-OCT-2001
60363222F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5212541 5',
mRNA sequence.
BI906283
BI906283.1 GI:16168946
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/
1 (bases 1 to 876)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11533 row: k column: 06
High quality sequence stop: 800.

RESULT 1
BI906283
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source

Location/Qualifiers
1. 876
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5212541"
/tissue_type="leukocyte"
/lab_host="DH10B"
/clone_lib="NIH MGC 118"
/note="Vector: PCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 21; DB 12; Length 876;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGAACTTATCGAATACA 21

DB 16 GCAGAACTTATCGAATACA 36

RESULT 2
BM150641
LOCUS

DEFINITION EST563164 PyBS Plasmodium yoelii yoelii cDNA clone PIC789 5' end, mRNA sequence.

ACCESSION BM150641.1 GI:17306322

VERSION EST

KEYWORDS Plasmodium yoelii yoelii

SOURCE Plasmodium yoelii yoelii

ORGANISM Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

REFERENCE 1 (bases 1 to 647)

AUTHORS Carleton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,A.B., Fraser,C.M. and Garucci,D.J.

TITLE Plasmodium yoelii EST project at TIGR

JOURNAL Unpublished (2001)

COMMENT Contact: Jane Carleton

Parasite Genomics Group

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-530-9319

Fax: 301-838-0208

Email: carleton@tigr.org

For clone info, please contact the Malaria Research and Reference

Reagent Resource Center, ATCC

http://www.malaria.mr4.org/mr4pages/index.html

Seq primer: ADP.

Location/Qualifiers

1. 647

/organism="Plasmodium yoelii yoelii"

/mol_type="mRNA"

/strain="17XL"

/sub_species="yoelii"

/db_xref="taxon:73239"

/clone="PYCJT89"

/dev_stage="Asexual blood stages"

/lab_host="E. coli XL-1 Blue"

/clone_lib="PyBS"

/notes="Vector: PAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/cByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose columns. Total RNA was isolated using the guanidinium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography."

FEATURES
source

Location/Qualifiers
1. 876
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5212541"
/tissue_type="leukocyte"
/lab_host="DH10B"
/clone_lib="NIH MGC 118"
/note="Vector: PCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."

First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to HyriZAP arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (pAD-GAL4) was excised from the HyriZAP vector and plasmid DNA isolated."

ORIGIN

Query Match 81.0%; Score 17; DB 12; Length 647;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GAACCTTATCGAATACA 21

DB 139 GAACCTTATCGAATACA 155

RESULT 3
AV340346
LOCUS

DEFINITION AV340346 RIKEN full-length enriched, adult male olfactory bulb Mus musculus cDNA clone 6430514H24 3', mRNA sequence.

ACCESSION AV340346

VERSION AV340346.1 GI:6380398

KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 288)

AUTHORS Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,T., Itch,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Takahashi,F., Tateo,M., Tomimaga,N., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yasunishi,A., Yokota,T., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.

TITLE RIKEN Mouse ESTs (Konno,H., et al. 1999)

JOURNAL Unpublished (1999)

COMMENT Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-resgsc.riken.go.jp

URL: http://genome.gsc.riken.go.jp/

Sasaki,N., Izawa,M., Watanabe,M., Ozawa,K., Tanaka,T., Yoneda,Y., Matsura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.

Transcriptional sequencing: A method for DNA sequencing using RNA

polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)

Ttoh,M., Kitsuina,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation

system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)

Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

Location/Qualifiers

1. 288

FEATURES
source

```

/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="6430314H24"
/sex="male"
/tissue_type="olfactory brain"
/dev_stage="adult"
/lab_hosts="DH10B"
/clone_lib="RIKEN full-length enriched, adult male
olfactory bulb"
/notes="Site 1: Sali; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 10.0 and subtraction to Rot = 100.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGAGATCTCGAGTAAATTAATATCCCCCCCCCCC
3']. cDNA was cloned into the XhoI and BamHI sites.
Vector: a modified pBluescript KS(+) after bulk excision
from Lambda FLC I. Cloning sites, 5' end: Sali; 3' end:
BamHI"

```

ORIGIN

```

Query Match      76.2%; Score 16; DB 9; Length 288;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 2 CAAGACTTATCGAAA 17

Db 41 CAAGACTTATCGAAA 56

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RESULT 4
BE344124      404 bp mRNA linear EST 10-MAR-2003
LOCUS      EST409286 potato stolon, Cornell University Solanum tuberosum cDNA
DEFINITION      clone CSTA28M16, mRNA sequence.
BE344124
ACCESSION      BE344124.1 GI:9253656
KEYWORDS      EST.
SOURCE      Solanum tuberosum (potato)
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.

```

```

REFERENCE
1 (bases 1 to 404)
van der Hoeven,R., Bezzerides,J., Bachem,C., Horvath,B., Visser,R.,
Holt,I.E., Liang,F., Hansen,T.S., Utterback,T., Bowman,C.L.,
Dean,B., Bougri,O., Buell,C.R., Ronning,C.M., Tanksley,S.D. and
Baker,B.
Generation of ESTs from potato swelling stolons
Unpublished (1999)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
Location/Qualifiers
1. .404
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Bintje"
/db_xref="taxon:4113"

```

FEATURES

```

source
1. .404
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Bintje"
/db_xref="taxon:4113"

```

```

/clone="CSTA28M16"
/tissue_type="axillary buds of stem explants, swelling
stolons"
/dev_stage="1 to 3 days"
/lab_host="SOLR"
/clone_lib="potato stolon, Cornell University"
/notes="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; RNA was supplied by Christian Bachem & Beatrice
Horvath(Laboratory of Plant Breeding, Dept. of Plant
Sciences, Wageningen University, The Netherlands). Total
RNA was isolated from developing axillary buds of potato
nodal stem cuttings cultured on medium for the
introduction of tuber formation as described in Bachem et
al. (Plant Journal 1996). Tissue samples were taken of
stages corresponding to growing stolons and the early
stages of tuber formation."

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ORIGIN

```

Query Match      76.2%; Score 16; DB 10; Length 404;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 3 AAGAACTTATCGAAAT 18

Db 88 AAGAACTTATCGAAAT 103

```

RESULT 5
BI179888      406 bp mRNA linear EST 10-MAR-2003
LOCUS      EST520833 cSTE Solanum tuberosum cDNA clone cSTE20F8 5' sequence,
DEFINITION      mRNA sequence.
BI179888
ACCESSION      BI179888.1 GI:14645699
KEYWORDS      EST.
SOURCE      Solanum tuberosum (potato)
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.

```

```

REFERENCE
1 (bases 1 to 406)
van der Hoeven,R., Bezzerides,J., Bachem,C., Visser,R., Cho,J.,
Chiemingo,A., Bougri,O., Buell,C.R., Ronning,C., Tanksley,S. and
Baker,B.
Generation of ESTs from in vitro grown microtubers
Unpublished (2001)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
Seq primer: M13F-R.
Location/Qualifiers
1. .406
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Bintje"
/db_xref="taxon:4113"
/clone="CSTE20F8"
/tissue_type="axillary buds of stem explants; growing
sink-tubers"
/dev_stage="7, 8 and 10 days"
/lab_host="SOLR"
/clone_lib="CSTE"
/notes="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; Tissue supplied by Christian Bachem and Richard
Visser (Department of Plant Breeding, Wageningen
University, The Netherlands). The cSTA libraries will
attempt to capture the induction and initiation/initial
growth of the tuber in an in vitro system as described in
Bachem et al. (Plant Journal, 1996). Small microtubers

```

develop from axillary buds attached to stem explants when placed on a high sucrose medium (10%). Visible morphological changes occur synchronously at day five in the axillary buds. The first library, cSTA (1-20) consists of axillary buds harvested on days 1-3. This targets those genes involved in induction of the microtubers. The following libraries, cSTA (21-40) and cSTA (41-60), capture genes involved in tuber initiation and outgrowth. This library is noted as P3 in Tanksley lab notebooks."

ORIGIN

Query Match 76.2%; Score 16; DB 12; Length 406;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGAACTTATCGAAAT 18

|||||
Db 90 AAGAACTTATCGAAAT 105

RESULT 6

BH743658/c

LOCUS

DEFINITION BH743658 477 bp DNA linear GSS 25-FEB-2002
ST25e07.b1 BoBuds01 Brassica oleracea genomic clone gt25e07 5',
Genomic survey sequence.

ACCESSION

BH743658

VERSION

BH743658.1

KEYWORDS

GSS.

SOURCE

Brassica oleracea

ORGANISM

Brassica oleracea

REFERENCE

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

AUTHORS

Katarai, M., O'Shaughnessy, A., Palmer, L., Bahret, A., Baker, J.,
Bailly, V., Cunniss, D.M., Katzenberger, P., King, L., Kirchoff, K.,
Kuit, K., Miller, B., Muller, S., Nascimento, L., Preston, R.,
Santos, L., Shah, R., Zutavern, T., Dedhia, N., Rabinowicz, P.D. and
McCombie, W.R.

TITLE

Whole Genome Shotgun Reads from Brassica oleracea (2002b)

JOURNAL

Unpublished (2002)

COMMENT

Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: gt25 row: e column: 07
Seq primer: -21UnivFwd
Class: shotgun
High quality sequence stop: 477.

FEATURES

Location/Qualifiers

1..477

/organism="Brassica oleracea"

/mol_type="genomic DNA"

/db_xref="taxon:3712"

/clone="gt25e07"

/clone_lib="BoBuds01"

/note="Vector: M13 for x reads, pBluescript for b and g
reads, Site_1: EcoRV; Whole genome shotgun library from
flowering buds. DNA was purified from a crude nuclear prep
using Brassica oleracea TO1000DH3 buds provided by Thomas
Osborn at the University of Wisconsin. Genomic DNA
provided by Pablo Rabinowicz (CSHL) and shotgun library
prepared in McCombie Lab."

ORIGIN

Query Match 76.2%; Score 16; DB 28; Length 477;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AAGAACTTATCGAAAT 19

|||||
Db 402 AGAACTTATCGAAAT 387

RESULT 7

BQ045539

LOCUS

DEFINITION

BQ045539 486 bp mRNA linear EST 10-MAR-2003
EST594656 P. infestans-challenged potato leaf, incompatible
reaction Solanum tuberosum cDNA clone BPL12K11 5' end, mRNA
sequence.

ACCESSION

BQ045539

VERSION

BQ045539.1

KEYWORDS

EST.

SOURCE

Solanum tuberosum (potato)

ORGANISM

Solanum tuberosum

REFERENCE

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.

AUTHORS

Zhang, P., Hernandez, M., Tornqvist, C.-E., Wirtz, U., Loukianov, A.,
Rangel, P., Haberlach, G.T., Karamecheva, S.A., Tsai, J., Chiemingo, A.,
Bouglri, O., Buell, C.R., Renning, C.M., Helgeson, J. and Baker, B.

TITLE

Generation of ESTs from Potato Leaves Challenged with Phytophthora
infestans, incompatible interaction (2002)

JOURNAL

Unpublished (2002)

COMMENT

Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
Seq primer: T3.

FEATURES

Location/Qualifiers

1..486

/organism="Solanum tuberosum"

/mol_type="mRNA"

/cultivar="Kennebec"

/db_xref="taxon:4113"

/clone="BPL12K11"

/tissue_type="leaf"

/dev_stage="6 week old"

/lab_host="SOLR"

/clone_lib="P. infestans-challenged potato leaf,
incompatible reaction"/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; supplier: UC Berkeley, PGEC; sequencing: The
Institute for Genomic Research. Whole plants were
challenged with 450,000 sporangia/ml P. infestans isolate
US-1 (US940501) in Biotron (Madison, Wisconsin). Leaf
tissue was collected at 1, 2, 5, 12, and 24 hours
post-challenge and frozen in liquid nitrogen immediately
upon removal. Kennebec plants showed no signs of HR.
Katahdin plants (susceptible to P. infestans US-1) were
used as controls and showed infection. NOTE: We cannot
exclude the possibility that this sequence is actually
derived from Phytophthora rather than potato."

ORIGIN

Query Match 76.2%; Score 16; DB 12; Length 486;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGAACTTATCGAAAT 18

|||||

Db 21 AAGAACTTATCGAAAT 36

ORIGIN

Query Match 76.2%; Score 16; DB 28; Length 477;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AAGAACTTATCGAAAT 19

ORIGIN

Query Match 76.2%; Score 16; DB 12; Length 486;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGAACTTATCGAAAT 18

|||||

Db 21 AAGAACTTATCGAAAT 36

ORIGIN

Query Match 76.2%; Score 16; DB 28; Length 477;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AAGAACTTATCGAAAT 19

```

ACCESSION      BB471486
VERSION        BB471486.1  GI:9561977
KEYWORDS
SOURCE         Solanum tuberosum (potato)
ORGANISM
REFERENCE
AUTHORS        van der Hoeven,R., Bezzerides,J., Bachem,C., Horvath,B., Visser,R.,
Holt,I.E., Liang,F., Hansen,T.S., Utterback,T., Bowman,C.L., and
Dean,B., Bougri,O., Buell,C.R., Ronning,C.M., Tanksley,S.D., and
Baker,B.
TITLE          Generation of ESTs from potato swelling stolons
JOURNAL
COMMENT        Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/.
FEATURES
Source
1..487
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Bintje"
/db_xref="taxon:4113"
/clone="CST29C12"
/tissue_type="axillary buds of stem explants, swelling
stolons"
/dev_stage="1 to 3 days"
/lab_host="SOLR"
/clone_lib="potato stolon, Cornell University"
/notes="Vector: pBlueScript SK(-); Site 1: EcoRI; Site 2:
XhoI; RNA was supplied by Christian Bachem & Beatrix
Horvath(Laboratory of Plant Breeding, Dept. of Plant
Sciences, Wageningen University, The Netherlands). Total
RNA was isolated from developing axillary buds of potato
nodal stem cuttings cultured on medium for the
introduction of tuber formation as described in Bachem et
al. (Plant Journal 1996). Tissue samples were taken of
stages corresponding to growing stolons and the early
stages of tuber formation."
ORIGIN
Query Match      76.2%; Score 16; DB 10; Length 487;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGAACTTATCGAAAT 18
|||||
DB 85 AAGAACTTATCGAAAT 100

RESULT 9
BX563981
LOCUS          BX563981 Glossina morsitans adult infected gut Glossina
DEFINITION    morsitans morsitans cDNA clone Tse6a02_q1c, mRNA sequence.
ACCESSION     BX563981
VERSION       BX563981.1  GI:33431183
KEYWORDS
SOURCE        Glossina morsitans morsitans
ORGANISM
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
1 (bases 1 to 493)
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
22881942
14519198
COMMENT        Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.
FEATURES
Source
1..493
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse6a02 q1c"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"
ORIGIN
Query Match      76.2%; Score 16; DB 13; Length 493;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGAACTTATCGAAAT 18
|||||
DB 28 AAGAACTTATCGAAAT 43

RESULT 10
BM407701
LOCUS          BM407701 517 bp mRNA linear EST 10-MAR-2003
DEFINITION    EST582028 potato roots Solanum tuberosum cDNA clone CPRO32A9 5'
end, mRNA sequence.
ACCESSION     BM407701
VERSION       BM407701.1  GI:18259331
KEYWORDS
SOURCE        Solanum tuberosum (potato)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 517)
van der Hoeven,R., Sun,H., Karamycheva,S.A., Tsai,J., Van Aken,S.,
Utterback,T., Chlamingo,A., Bougri,O., Buell,C.R., Ronning,C.,
Tanksley,S. and Baker,B.
Generation of ESTs from potato roots
Unpublished (2001)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
Seq primer: T3
FEATURES
Source
1..517
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="CPRO32A9"

```

/tissue_type="roots"
/dev stage="in vitro grown stem cuttings"
/lab_host="SOLR"
/clone_lib="potato roots"

/notes=Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; supplier: Cornell University, Tanksley lab; sequencing: The Institute for Genomic Research. Roots were isolated from in vitro grown stem cuttings on CM medium. Roots were isolated two weeks after placing the stem cuttings from in vitro grown plants on medium."

ORIGIN

Query Match 76.2%; Score 16; DB 12; Length 517;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGAACTTATCGAAT 18

Db 43 AAGAACTTATCGAAT 58

RESULT 11

BI435938

LOCUS

DEFINITION EST38699 cSTD Solanum tuberosum cDNA clone cSTD20L16 5' sequence,
mRNA sequence.

ACCESSION

BI435938

VERSION

BI435938.1

KEYWORDS

SOURCE

ORGANISM

Solanum tuberosum (potato)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
Seq primer: MJ3P-R.

FEATURES

source

1..649
/location/Qualifiers
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cSTD20L16"
/tissue_type="dormant tuber"
/dev stage="one month post-harvest"
/lab host="SOLR"
/clone_lib="cSTD"

/note=Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; This library targets genes expressed in dormant tubers. This library was made from sections of dormant tuber, avoiding the buds and epidermis. Tubers were stored for one month post-harvest at 40C. The tuber was peeled, well away from the surface. Then it was chopped into 1-2 mm cubes and immediately frozen in liquid nitrogen. This library is noted as P4 in Tanksley lab notebooks."

ORIGIN

Query Match 76.2%; Score 16; DB 12; Length 649;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGAACTTATCGAAT 18

Db

RESULT 12

CA998937

LOCUS

DEFINITION

ACCESSION

CA998937

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Benildo G. de los Reyes

Plant Genomics Lab., Department of Crop, Soil and Environmental
Sciences
University of Arkansas
115 Plant Science Building, Fayetteville, AR 72701, USA
Tel: (479)-575-7465
Fax: (479)-575-8435
Email: breyes@uark.edu
Plate: S345S row: B column: 01
Seq primer: T3.

FEATURES

source

1..654
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="PI560247"
/db_xref="taxon:39947"
/tissue_type="coleotile, radicle, prophyll, immature leaf"
/dev stage="embryo at different stages of germination and
shoots of germinated seeds under chilling stress
(130C/100C)"
/lab host="Solr"
/clone_lib="Rice cold stress germination cDNA library"
/note=Organ: seedlings; Vector: Lambda Uni-Zap XR excised
as pBluescript; Site 1: EcoRI; Site 2: XhoI; The cDNAs
were derived from reverse transcription of mRNA samples
from seeds at different stages of germination and
seedlings at early phase of growth under chilling stress
(130C/100C). The mRNA pool was used as template for double
stranded cDNA synthesis using the Stratagene Uni-Zap XR
cDNA synthesis and library kit. A total of 150,000 phages
were excised from the primary library as pBluescript
phagemid clones. Enrichment of the primary excised library
with chilling-induced transcripts was performed by
hybridizing the primary excised library colony lifts with
the PCR-select subtraction product, with cold germinated
cDNA as tester and control temperature-germinated cDNA as
driver."

ORIGIN

Query Match 76.2%; Score 16; DB 14; Length 654;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAAGAACTTATCGAAA 17

Db 35 CAAGAACTTATCGAAA 50

RESULT 13

```

BI435917      B1435917      677 bp      mRNA      linear      EST 10-MAR-2003
LOCUS      EST538678 cSTD Solanum tuberosum cDNA clone cSTD20F8 5' sequence,
DEFINITION      mRNA sequence.
ACCESSION      B1435917
VERSION      B1435917.1 GI:15260607
KEYWORDS      EST.
SOURCE      Solanum tuberosum (potato)
ORGANISM      Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanaceae; Solanum.
REFERENCE      1 (bases 1 to 677)
AUTHORS      van der Hoeven,R., Bezzerides,J., Ewing,E., Cho,J., Chiemiango,A.,
Bougri,O., Buell,C.R., Renning,C., Tanksley,S. and Baker,B.
TITLE      Generations of ESTs from dormant potato tubers
JOURNAL      Unpublished (2001)
COMMENT      Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
Seq primer: M13F-R.
FEATURES             source
1..677
    /organism="Solanum tuberosum"
    /mol_type="mRNA"
    /cultivar="Kennebec"
    /db_xref="taxon:4113"
    /clone="cSTD20F8"
    /tissue_type="dormant tuber"
    /dev_stage="one month post-harvest"
    /lab_host="SOLR"
    /clone_lib="cSTD"
    /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; This library targets genes expressed in dormant
tubers. This library was made from sections of dormant
tuber, avoiding the buds and epidermis. Tubers were stored
for one month post-harvest at 40C. The tuber was peeled,
well away from the surface. Then it was chopped into 1-2
mm cubes and immediately frozen in liquid nitrogen. This
library is noted as P4 in Tanksley lab notebooks."
ORIGIN
    Query Match      76.2%; Score 16; DB 12; Length 677;
    Best Local Similarity 100.0%; Pred. No. 69;
    Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 AAGAACTTATCGAAAT 18
      |||||
DB      90 AAGAACTTATCGAAAT 105

RESULT 14
B2387666/c
LOCUS      B2387666      685 bp      DNA      linear      GSS 30-APR-2003
DEFINITION      EIND95TF EI_10_12_KB Entamoeba invadens genomic clone EIND95,
genomic survey sequence.
ACCESSION      B2387666
VERSION      B2387666.1 GI:30234203
KEYWORDS      GSS
SOURCE      Entamoeba invadens
ORGANISM      Entamoeba invadens
Eukaryota; Entamoebidae; Entamoeba.
REFERENCE      1 (bases 1 to 685)
AUTHORS      Wang,Z., Samuelson,J., Clark,C.G., Eichinger,D., Paul,J., van
Dellen,K., Hall,N., Anderson,I. and Lofus,B.
TITLE      Geie discovery in the Entamoeba invadens genome
JOURNAL      Mol. Biochem. Parasitol. 129 (1), 23-31 (2003)
MEDLINE      22684048
PUBMED      12798503

```

```

Other GSSs: EIND95TR
Contact: Brendan Loftus
Department of Eukaryotic Genomics
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: enta@tigr.org
DNA was provided by Daniel Eichinger
Seq primer: TF
Class: Sheared ends.
FEATURES             source
1..685
    /organism="Entamoeba invadens"
    /mol_type="genomic DNA"
    /strain="IP-1"
    /db_xref="taxon:33085"
    /clone="EIND95"
    /clone_lib="EI_10_12_KB"
    /note="Vector: pHOS2; Site_1: BstXI; Total genomic DNA was
isolated from early log phase trophozoites of E. invadens
IP-1 using a Qiagen plant DNA extraction kit. A shotgun
medium-size plasmid library (average insert size of 10 -
12 kb) was generated by random mechanical shearing of E.
invadens genomic DNA, repairing the ends of DNA fragments
with T4 Polymerase, adding BstXI adaptors and ligating
into the BstXI site of a pUC-derived vector pHOS2."
ORIGIN
    Query Match      76.2%; Score 16; DB 28; Length 685;
    Best Local Similarity 100.0%; Pred. No. 69;
    Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 AAGAACTTATCGAAAT 18
      |||||
DB      22 AAGAACTTATCGAAAT 7

RESULT 15
BG031536
LOCUS      BG031536      694 bp      mRNA      linear      EST 24-JAN-2001
DEFINITION      602299367F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4393720 5',
mRNA sequence.
ACCESSION      BG031536
VERSION      BG031536.1 GI:12421916
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 694)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10088 row: e column: 17
High quality sequence stop: 612.
FEATURES             source
1..694
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="IMAGE:4393720"
    /tissue_type="mammary adenocarcinoma, cell line"
    /lab_host="DH10B (phage-resistant)"

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/clone lib="NIH_MGC 87"
/notes="Organ: breast; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.383 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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ORIGIN

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Query Match      76.2%; Score 16; DB 10; Length 694;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      3  AAGAACTTATCGAAAT 18
         |||||
Db      469 AAGAACTTATCGAAAT 484
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Search completed: August 2, 2004, 20:28:09
Job time : 871.879 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 19:08:00 ; Search time 106.267 Seconds
(without alignments)
968.934 Million cell updates/sec

Title: US-10-068-067-19

Perfect score: 21
Sequence: 1 gcaagaacttcgaaataca 21

Scoring table: OIRGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3222919 seqs, 2451570024 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6445838

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:

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- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq*
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- 17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq*
- 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq*
- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	21	100.0	21	14	US-10-068-067-24
3	21	100.0	51	14	US-10-068-067-16
4	21	100.0	51	14	US-10-068-067-21
5	21	100.0	1193	15	US-10-283-028-3
6	21	100.0	2895	14	US-10-068-067-11
7	17	81.0	11124	14	US-10-108-605-286
8	17	81.0	11184	14	US-10-108-605-284
9	16	76.2	465	17	US-10-437-963-67946
10	16	76.2	1761	17	US-10-437-963-67947
11	15	71.4	537	10	US-09-991-936-1052
12	15	71.4	1500	16	US-10-369-493-46193
13	15	71.4	1556	17	US-10-437-963-52116
14	15	71.4	1674	9	US-09-938-842A-665

c	15	71.4	1674	11	US-09-938-842A-665	Sequence 665, App
16	14	66.7	158	13	US-10-424-599-86155	Sequence 86155, A
c	17	66.7	247	17	US-10-437-963-30059	Sequence 30059, A
18	14	66.7	479	13	US-10-240-425-1360	Sequence 1360, Ap
19	14	66.7	495	13	US-10-027-632-94597	Sequence 94597, A
20	14	66.7	495	13	US-10-027-632-305493	Sequence 305493, A
21	14	66.7	495	16	US-10-027-632-94597	Sequence 94597, A
22	14	66.7	495	16	US-10-027-632-305493	Sequence 305493, A
c	23	66.7	564	13	US-10-282-122A-17492	Sequence 17492, A
c	24	66.7	575	13	US-10-424-599-76184	Sequence 76184, A
25	14	66.7	672	9	US-09-770-149-565	Sequence 565, App
26	14	66.7	714	13	US-10-282-122A-38551	Sequence 38551, A
c	27	66.7	714	13	US-10-424-599-107802	Sequence 107802, A
28	14	66.7	898	10	US-09-841-260-138	Sequence 138, App
29	14	66.7	898	14	US-10-007-693-138	Sequence 138, App
30	14	66.7	898	17	US-10-762-058-138	Sequence 138, App
31	14	66.7	1023	16	US-10-369-493-44068	Sequence 44068, A
32	14	66.7	1026	16	US-10-369-493-30362	Sequence 30362, A
33	14	66.7	1079	16	US-10-369-493-30362	Sequence 30362, A
34	14	66.7	1338	13	US-10-282-122A-12435	Sequence 12435, A
35	14	66.7	1366	13	US-10-282-122A-37797	Sequence 37797, A
c	36	66.7	1848	17	US-10-437-963-102418	Sequence 102418, A
c	37	66.7	2177	16	US-10-437-963-515-3	Sequence 3, Appli
c	38	66.7	2238	13	US-10-424-599-2236	Sequence 2236, Ap
c	39	66.7	2354	10	US-09-841-260-137	Sequence 137, App
c	40	66.7	2354	14	US-10-007-693-137	Sequence 137, App
c	41	66.7	2354	17	US-10-762-058-137	Sequence 137, App
42	14	66.7	2424	16	US-10-369-493-45830	Sequence 45830, A
43	14	66.7	3674	17	US-10-437-963-63590	Sequence 63590, A
c	44	66.7	3900	17	US-10-437-963-88074	Sequence 88074, A
45	14	66.7	4820	13	US-10-158-844-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-10-068-067-19
; Sequence 19, Application US/10068067
; Publication No. US20020151064A1
; GENERAL INFORMATION:
; APPLICANT: Rothenberg, Marc E.
; APPLICANT: Zimmermann, Nives
; TITLE OF INVENTION: REGULATION OF CCR3 EXPRESSION
; FILE REFERENCE: CWC-153
; CURRENT APPLICATION NUMBER: US/10/068, 067
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 60/267,073
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-068-067-19

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Best Local Similarity 100.0%; Pred. No. 0.0077;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGAAGCTTATCGAAATACA 21
Db 1 GCAAGAAGCTTATCGAAATACA 21

RESULT 2

US-10-068-067-24
; Sequence 24, Application US/10068067
; Publication No. US20020151064A1
; GENERAL INFORMATION:
; APPLICANT: Rothenberg, Marc E.

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGAACTTATCGAATAACA 21
Db 15 GCAAGAACTTATCGAATAACA 35

RESULT 6

US-10-068-067-11
; Sequence 11, Application US/10068067
; Publication No. US20020151064A1
; GENERAL INFORMATION:
; APPLICANT: Rothenberg, Marc E.
; APPLICANT: Zimmermann, Nives
; APPLICANT: Children's Hospital Medical Center
; TITLE OF INVENTION: REGULATION OF CCR3 EXPRESSION
; FILE REFERENCE: CMC-153
; CURRENT APPLICATION NUMBER: US/10/068,067
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 60/267,073
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 2895
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-068-067-11

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Best Local Similarity 100.0%; Pred. No. 0.0098;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGAACTTATCGAATAACA 21
Db 1591 GCAAGAACTTATCGAATAACA 1611

RESULT 7

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; Sequence 286, Application US/10108605
; Publication No. US20020160934A1
; GENERAL INFORMATION:
; APPLICANT: Broadus, Julie
; APPLICANT: Stam, Lynn
; APPLICANT: Bachmann, Jane
; APPLICANT: Kamdar, Kim
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
; FILE REFERENCE: 31133B
; CURRENT APPLICATION NUMBER: US/10/108,605
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US 09/761,142
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/176,418
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 286
; LENGTH: 11124
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-10-108-605-286

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Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGAACTTATCGAATAA 19
Db 3529 AAGAACTTATCGAATAA 3513

RESULT 8

US-10-108-605-284/c
; Sequence 284, Application US/10108605
; Publication No. US20020160934A1
; GENERAL INFORMATION:
; APPLICANT: Broadus, Julie
; APPLICANT: Stam, Lynn
; APPLICANT: Bachmann, Jane
; APPLICANT: Kamdar, Kim
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
; FILE REFERENCE: 31133B
; CURRENT APPLICATION NUMBER: US/10/108,605
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US 09/761,142
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/176,418
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 284
; LENGTH: 11184
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-10-108-605-284

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Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGAACTTATCGAATAA 19
Db 3589 AAGAACTTATCGAATAA 3573

RESULT 9

US-10-437-963-67946
; Sequence 67946, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 67946
; LENGTH: 465
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_68757C.1
US-10-437-963-67946

Query Match 76.2%; Score 16; DB 17; Length 465;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAAGAACTTATCGAAA 17
Db 120 CAAGAACTTATCGAAA 135

RESULT 10

US-10-437-963-67947/c

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; Sequence 67947, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 46193
; LENGTH: 1500
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-46193

Query Match 71.4%; Score 15; DB 16; Length 1500;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 237 GCAGAACTTATCGA 251

RESULT 13
US-10-437-963-52116
; Sequence 52116, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 52116
; LENGTH: 1556
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_54443C.1
US-10-437-963-52116

Query Match 71.4%; Score 15; DB 17; Length 1556;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAAGAACTTATCGAA 16
DB 777 CAAGAACTTATCGAA 791

RESULT 14
US-09-938-842A-665/c
; Sequence 665, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun

; Sequence 67947, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 67947
; LENGTH: 1761
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_68758C.1
US-10-437-963-67947

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Best Local Similarity 100.0%; Pred. No. 9;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAAGAACTTATCGAAA 17
DB 1265 CAAGAACTTATCGAAA 1250

RESULT 11
US-09-991-936-1052
; Sequence 1052, Application US/09991936
; Publication No. US20030073827A1
; GENERAL INFORMATION:
; APPLICANT: Brandt, Kevin S.
; APPLICANT: Gaines, Patrick J.
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: FLEA HEAD, NERVE CORD, HINDGUT AND MALPIGHIAN TUBULE
; FILE REFERENCE: PC-6-C1
; CURRENT APPLICATION NUMBER: US/09/991,936
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US/09/543,668
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/128,704
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1959
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1052
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Ctenocephalides felis
US-09-991-936-1052

Query Match 71.4%; Score 15; DB 10; Length 537;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AACTTATCGAATAC 20
DB 144 AACTTATCGAATAC 158

RESULT 12
US-10-369-493-46193
; Sequence 46193, Application US/10369493
; Publication No. US20030233675A1
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; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 665
; LENGTH: 1674
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-665

Query Match 71.4%; Score 15; DB 9; Length 1674;
Best Local Similarity 100.0%; Pred.No.35;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 563 AACTTATCGAAATAC 549

RESULT 15
US-09-938-842A-665/c
; Sequence 665, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 665
; LENGTH: 1674
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-665

Query Match 71.4%; Score 15; DB 11; Length 1674;
Best Local Similarity 100.0%; Pred.No.35;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AACTTATCGAAATAC 20
|||||
DB 563 AACTTATCGAAATAC 549

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Job time : 107.267 secs

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